

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 04:07:05 ; Search time 2691 Seconds

(without alignments)
7912.202 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aatatcatcattatca.....tgttgcaggagaaaaaaa 713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_hcc.*

9: gb_estl.*

10: gb_est2.*

11: gb_hcc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_eston.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_man.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	527.8	74.0	663	9 AU185777	AU185777 AU185777
C 2	268.2	37.6	800	14 CB958894	CB958894 AGENCOURT
C 3	147.6	20.7	663	28 AZ121459	AZ121459 RPCI-23-3
C 4	138.4	19.4	659	12 BI018962	BI018962 IL3-MT026

5	120	16.8	673	9	AV721179	AV721179
6	104.8	14.7	582	14	CB420818	CB420818 S93806 MA
7	76.6	10.7	363	13	BY547544	BY547544 BY547544
8	76.6	10.7	419	13	BY536666	BY536666 BY536666
9	73.8	10.4	855	12	BI107684	BI107684 602891529
C 10	58.6	8.2	1101	29	CNS0039G	AL063921 Drosophil
11	56	7.9	427	13	BX403499	BX403499 BX403499
12	56	7.9	759	29	CNS06QXV	AL411257 T7 end of
13	55.6	7.8	996	29	CNS00FUH	AL071063 Drosophil
14	54.2	7.6	895	29	CNS06FSV	AL396821 T7 end of
C 15	54	7.5	1043	29	CNS0145P	AL103735 Drosophil
C 16	53.4	7.5	1099	13	BX456575	BX456575 BX456575
17	53.2	7.5	583	29	CNS04AQC	AL274417 Tetradon
C 18	52.8	7.4	1029	29	CNS01XGM	AL174271 Tetradon
C 19	52.2	7.3	1010	13	BX363969	BX363969 BX363969
C 20	51.8	7.3	909	13	BX391298	BX391298 BX391298
C 21	51.4	7.2	661	29	AG160661	AG160661 Pan trogl
C 22	51.2	7.2	928	29	CNS00DKY	AL071865 Drosophil
C 23	50.2	7.0	1164	14	CF661469	CF661469 CcLL10a35
24	50	7.0	1184	29	CNS04PAP	AL300850 Tetradon
25	49.8	7.0	1182	9	AL513719	AL513719 AU513719
C 26	49.8	7.0	1201	13	BX443774	BX443774 BX443774
C 27	49.6	7.0	994	13	BX414650	BX414650 BX414650
C 28	49.6	7.0	1204	29	CNS016E2	AL106628 Drosophil
C 29	49.4	6.9	460	12	BI814616	BI814616 PFESTOaa4
C 30	49.4	6.9	1225	29	CNS0161D	AL106171 Drosophil
C 31	49.2	6.9	1201	13	BX360615	BX360615 Drosophil
32	49	6.9	987	29	CNS014PQ	AL104456 Drosophil
C 33	48.8	6.8	1201	9	AL532464	AL532464 AL532464
34	48.6	6.8	452	13	BX446269	BX446269 BX446269
35	48.6	6.8	734	29	CNS010MP	AL099163 Drosophil
36	48.6	6.8	1201	9	AL581406	AL581406 AL581406
37	48.6	6.8	1201	13	BX355654	BX355654 BX355654
38	48.6	6.8	1201	13	BX439779	BX439779 BX439779
39	48.6	6.8	1201	13	BX446296	BX446296 BX446296
C 40	48.4	6.8	1101	29	CNS017KX	AL108171 Drosophil
C 41	48.4	6.8	1201	9	AL536104	AL536104 AL536104
C 42	48.2	6.8	1163	13	BX462115	BX462115 BX462115
C 43	48	6.7	1391	29	CG754863	CG754863 P050-2-GO
44	47.6	6.7	524	12	BM883775	BM883775 rc22f10.y
45	47.6	6.7	527	12	BM883968	BM883968 rc24h04.y

ALIGNMENTS

RESULT 1

AU185777/c

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens
cDNA clone B02302-019, mRNA sequence.
663 bp mRNA linear EST 05-JUL-2001

AU185777.1 GI:14623690

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 663)

Sugita, Y., Oshida, T. and Oya, Y.

Human cDNA sequencing

Unpublished (2001)

Contact: Yuji Sugita

Genex Research, Inc.

907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan

Tel: 81-44-797-2281

Fax: 81-44-797-2622

Email: syuji@genex.co.jp, URL: http://www.genex.co.jp.

Location/Qualifiers

1. .663

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

FEATURES
source

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/clone="B02302-019"
/cell_type="Mast cell"
/clone_lib="Homo sapiens Mast cell library (Sugita Y)"

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Query Match      74.0%; Score 527.8; DB 9; Length 663;
Best Local Similarity 95.3%; Pred. No. 1.6e-92;
Matches 573; Conservative 0; Mismatches 23; Indels 5; Gaps 3;

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Qy 2 ATATATCATCTATTATCATTAATCAATTAATGTTCTTTTATTCCTAATAACATTTGGGT 61
Db 597 AAATATCATCTATTATCATTAATCAATTAATGTTCTTTTATTCCTAATAATTTGGGT 538
Qy 62 TTTGGGATTTTAAATTTTCAACACAGCAGGATGACATTTTCTGTCACATTAATTTG 121
Db 537 TTGGGGATTTTAAATTTTCAACACAGCAGGATGACATTTTCTGTCACATTAATTTG 478
Qy 122 TTGGTATGTAAGCTATTGTTG-AGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 180
Db 477 TTGGTATGTAAGCTATTGTTG-AGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 421
Qy 181 CTTTCTATCAGAAATAAAGAGAACCCAGTCAGTCAACCCACACATTCATCTTTAGAGACAG 240
Db 420 CTTTCTATCAGAAATAAAGAGAACCCAGTCAGTCAACCCACACATTCATCTTTAGAGACAG 361
Qy 241 TGTGACTCTACCAAGCTGTCACACACAGGCAAGGATAGTTAAAGACGGAATCT 300
Db 360 TG-GACTCTCTACCAAGCTGTCACACACAGGCAAGGATAGTTAAAGACGGAATCT 302
Qy 301 TGACTCAAGAGGGTTAAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGTAAAGAAAACAC 360
Db 301 TGACTCAAGAGGGTTAAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGTAAAGAAAACAC 242
Qy 361 TTAGATTCATGATTGTTAAATTTAAGGCAATATACATATTAGTATTACCTTAGTGTAA 420
Db 241 TTAGATTCATGATTGTTAAATTTAAGGCAATATACATATTAGTATTACCTTAGTGTAA 182
Qy 421 GTATCCCTGTCATATATACATTAAGTCAAGTCAATTAAGTCAAGTCAAGTCAAGTCAAG 480
Db 181 GTATCCCTGTCATATATACATTAAGTCAAGTCAATTAAGTCAAGTCAAGTCAAGTCAAG 122
Qy 481 AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGATTTATCCTGCTATGT 540
Db 121 AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGATTTATCCTGCTATGT 62
Qy 541 GCTTAGATCTACAGAGATCATATATTGATACAAATAAAGAAAAGTTCTCTCC 600
Db 61 GCTTAGATCTACAGAGATCATATATTGATACAAATAAAGAAAAGTTCTCTCC 2
Qy 601 T 601
Db 1 T 1

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RESULT 2
CB958894
LOCUS
DEFINITION
AGENCY 13785021 NIH MGC 184 Homo sapiens CDNA clone
IMAGE:30352338 5', mRNA sequence.
ACCESSION
CB958894
VERSION
CB958894.1 GI:30215010
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 800)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

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```

CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM151 row: e column: 19
High quality sequence stop: 488.
Location/Qualifiers
source
1.800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352338"
/clone_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggcattatggc); Site_2: SfiI (ggcgcctggc);
SfiI (ggcattatggc); and 3' adaptor sequence:
5'-CACGGCCATATGCG-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

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FEATURES
source
1.800
Location/Qualifiers

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Query Match      37.6%; Score 268.2; DB 14; Length 800;
Best Local Similarity 98.9%; Pred. No. 3e-42;
Matches 270; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 AATATATCATCTATTATTCATTAATCAATTAATGTTCTTTTATTCCTAATAACATTTGGG 60
Db 251 AATATATCACTATTATTCATTAATCAATTAATGTTCTTTTATTCCTAATAACATTTGGG 310
Qy 61 TTTTGGGATTTTAAATTTTCAACACAGAGATGACATTTTCTGTCACATTAATTTAT 120
Db 311 TTTTGGGATTTTAAATTTTCAACACAGAGATGACATTTTCTGTCACATTAATTTAT 370
Qy 121 GTTGTATGTAAGCTATTGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 180
Db 371 GTTGTATGTAAGCTATTGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 430
Qy 181 CTTTCTATCAGAAATAAAGAGAACCCAGTCAGTCAACCCACACATTCATCTTTAGAGACAG 240
Db 431 CTTTCTATCAGAAATAAAGAGAACCCAGTCAGTCAACCCACACATTCATCTTTAGAGACAG 490
Qy 241 TGTGACTCTCTACCAAGCTGTCAAAACACACAGG 273
Db 491 TGTGACTCTCTACCAAGCTGTCAAAACACACAGG 523

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RESULT 3
AZ121459/c
LOCUS
DEFINITION
PCPI-23-30A15.TV PCPI-23 Mus musculus genomic clone PCPI-23-30A15,
genomic survey sequence.
ACCESSION
AZ121459
VERSION
AZ121459.1 GI:7788387
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 663)
AUTHORS
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., McGann, S., Tseng, G., Geer, K., Krol, M., de
Jong, P., and Fraser, C.M.
TITLE
Mouse BAC End Sequences from Library PCPI-23

```

JOURNAL
COMMENT

Unpublished (1999)
Other GSSs: RPCI-23-30A15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetec (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac/bac_ends/mouse/bac_end_intro.html
Plate: 30 row: A column: 15
Seq primer: T7
Class: BAC ends.

FEATURES
source

1..663
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-30A15"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 20.7%; Score 147.6; DB 28; Length 663;
Best Local Similarity 71.6%; Pred. No. 7.3e-19;
Matches 252; Conservative 0; Mismatches 89; Indels 11; Gaps 4;
QY 1 AATATATCATCTATTATTCATTAATCAATATGATTTCT-TTATTCATCAATATGTTGG 59
Db 351 AACATACAGTTTATTTATCAATACCAATGCGCATCCCTATATATATGCTTAAATATGA 292
QY 60 GTTTGGGATTTTAAATTTCAACACAGCAGATGACAT-TTTTCTGTCATTTATT 117
Db 291 GTGCTGGCATTTCCATTTTAAACACAGCAGATGATCTTTCTTTTCTGTCATTTGCT 232
QY 118 ATTGTTGGTATGTAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGG 177
Db 231 GTTCGTGACGTATCAAGCAATTTTGTGCACAAATTCAGGGAGAATCCAGAGGAGAAAA 172
QY 178 CTACTTTCTATCAGAAATTAAGAGACCAAGTCACAGTCACACCAATCATCTTTAGAGA 237
Db 171 CAATCTTCTATCAAGAAATTAAGAGAACCA--AGCCCCACAGAAATCATCTTTAGATGA 115
QY 238 CAGTGTGACTCTACCAAGCTGTCAAAACACAGGCAAGGGCATAGTTAAAGCA---- 292
Db 114 GAAGTGTGCTCCCTCCAGGCATCCCAACTACAGGCAAGGGCAGGCAAGAGGCAAT 55
QY 293 CGGAATCTTGACTCAAGAGGTTTAAATTTCTTGGTCTGAAGCCTGGGGCAGGG 344
Db 54 GGGATCCCGGATTCAGAGGTTTCATTTCTGCTGAGGCTGGGGTGGGG 3

RESULT 4
BI018962/c

LOCUS BI018962
DEFINITION IL3-MT0267-050101-437-A02 MT0267 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI018962
VERSION BI018962.1 GI:14425592
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 659)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

PubMed

10737800

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&et2=IL3-MT0267-050101-437-A02&t3=2001-01-05&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 639.

FEATURES

source
1..659
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0267"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 19.4%; Score 138.4; DB 12; Length 659;
Best Local Similarity 99.3%; Pred. No. 4.4e-17;
Matches 139; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 134 GCTATTGGAGATCCCAATTCAGGAAGCAACACATTCGAGATGCTACTTTCTATCAAGA 193
Db 572 GCTATTGGAGTCCCAATTCAGGAAGCAACACATTCGAGATGCTACTTTCTATCAAGA 513
QY 194 AATAAGAGAACCAAGTCACACCAATCATCTTTAGAGACAGTGTGACTCTTACC 253
Db 512 AATAAGAGAACCAAGTCACACCAATCATCTTTAGAGACAGTGTGACTCTTACC 453
QY 254 AAAGCTGTCAAAACCAAGCAGG 273
Db 452 AAAGCTGTCAAAACCAAGCAGG 433

RESULT 5

AV7211179
LOCUS AV7211179 HTB Homo sapiens cDNA clone HTBAKF11 5', mRNA sequence.
DEFINITION AV7211179
ACCESSION AV7211179
VERSION AV7211179.1 GI:10818331
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Gu, Y., Peng, Y., Gong, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzge@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
      source
      1..673
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="HTBAKFl1"
      /tissue_type="Hypothalamus"
      /dev_stage="Adult"
      /lab_host="SOLR"
      /clone_lib="HTB"
      /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
      XhoI"

ORIGIN
Query Match      16.8%; Score 120; DB 9; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 AGGAAGCAACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACCAAGTCA 213
Db 1 AGGAAGCAACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACCAAGTCA 60

Qy 214 ACCCACAAATCATCTTTAGAGACAGGTGCTACCTCAACCAAGCTGTCRAAACCAAGG 273
Db 61 ACCCACAAATCATCTTTAGAGACAGGTGCTACCTCAACCAAGCTGTCRAAACCAAGG 120

RESULT 6
CB420818          582 bp  mRNA  linear  EST 25-MAR-2003
DEFINITION      593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION      CB420818
VERSION        CB420818.1  GI:29187264
KEYWORDS       EST.
SOURCE         Bos taurus (cow)
ORGANISM       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 582)
Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keeler, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plater, FQY8014 row: B column: 7
Seq primer: GTAATACGATCCTACATAGG.

FEATURES
      source
      1..582
      /organism="Bos taurus"
      /mol_type="mRNA"
      /db_xref="taxon:9913"
      /tissue_type="pooled"
      /lab_host="DH10B"
      /clone_lib="MARC 6BOV"
      /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
      Library made with RNA pooled from multiple tissues
      including liver, lung, hypothalamus, pituitary, and
      placenta/endometrium."

ORIGIN
Query Match      14.7%; Score 104.8; DB 14; Length 582;
Best Local Similarity 84.3%; Pred. No. 1.5e-10;
Matches 118; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 134 GCTATTTGGAGATCCAAATTCAGGAAGCAACACATTCGGAATGGCTACTTTCTATCAAGA 193
Db 244 GGTATTTGGAGATCCAGTTCAGGGAACAACCTGTTGAAGAGTGACAGCTTTCCATCAAGA 303

Qy 194 AATAAGAGAACCAACAGTCACCCACCAATCATCTTTAGAGACAGTGTGACTCTTACC 253
Db 304 AATAAGAGAACCAACAGTGTGACCCACCAATCATCTTTAGAGATAGTGTGATACCTTACC 363

Qy 254 AAGCTGTCAAAACCAACAGG 273
Db 364 AAGCTGTCAACCAACAGG 383

RESULT 7
BY547544          363 bp  mRNA  linear  EST 14-DEC-2002
DEFINITION      BY547544 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
cells Mus musculus cDNA clone F73011908 3', mRNA sequence.
ACCESSION      BY547544
VERSION        BY547544.1  GI:26881923
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 363)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Buit, C.,
Hume, D.A., Quackenbush, J., Schriml, D.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.O., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, R., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
MEDLINE

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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
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Db 291 GTGCTGCAATTTCCATTTTAAACACACAGCAGATGACATTTCTTTTCTGTCACATTTGCT 350
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LOCUS
DEFINITION
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BI107684
BI107684.1 GI:14558577
EST.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 855)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LWA1101 row: j column: 08
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High quality sequence stop: 825.
Location/Qualifiers
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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QY 253 CAAAGCTGTCAAAACACACAGG 273
Db 427 CAAGGCATCCAACTACAGG 447

RESULT 10
CNS00396/c
LOCUS

DEFINITION
CNS00396 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence NEST3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL063921
AL063921.1 GI:4941778
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammose in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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Db 546 GAAAAAAAAARAGAGAAAAAAAAASAA 519

Search completed: April 4, 2004, 06:03:36
Job time : 2705 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 06:04:01 ; Search time 406 Seconds
(without alignments)

6568.364 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aaatatacatctattatca.....tggtgcaaggaagaaaaaaa 713

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Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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ALIGNMENTS

RESULT 1

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; Sequence 376 Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Forgy, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C63

; CURRENT APPLICATION NUMBER: US/09/989,722

; CURRENT FILING DATE: 2001-11-19

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; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 713; DB 9; Length 713;
 Best Local Similarity 100.0%; Pred. No. 5e-161;
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QY 61 TTTTGGGATTTTAAATTTTCAACACACAGAGATGACATTTTCTGTCTACCTATTATTATT 120
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 Db 61 TTTTGGGATTTTAAATTTTCAACACACAGAGATGACATTTTCTGTCTACCTATTATTATT 120
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QY 121 GTTGTATGTGAAGCTATTTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
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 Db 121 GTTGTATGTGAAGCTATTTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
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RESULT 3
US-09-989-279-376
Sequence 376 Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989, 279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16

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RESULT 4

US-09-989-727-376
Sequence 376, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 5e-161;
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; GENERAL INFORMATION:
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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 ; PRIOR FILING DATE: 1998-07-09

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us-09-989-293a-376.rnpb

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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 5e-161;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14

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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-07-09

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DB 541 GCTTAGATCTACAGGAGATCAATATTTGATACAAATTAAGAAAGAGTTCTCTCCCC 600

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DB 601 TTACAGAAATTCACATTTTAAATCGGATACACATTTAGTAAATAGGAAATTCACATTAGAAAG 660

QY 661 AAGAAATCAGAGGAGAAAGGAAAGAGGAAATTTGCCAGGAAAAA 713
DB 661 AAGAAATCAGAGGAGAAAGGAAAGAGGAAATTTGCCAGGAAAAA 713

RESULT 13
US-09-992-598-376
; Sequence 376, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20

1 ; CURRENT APPLICATION NUMBER: US/09/992,598
2 ; CURRENT FILING DATE: 2001-11-14
3 ; PRIOR APPLICATION NUMBER: 60/049787
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, PRIOR FILING DATE: 1998-07-02
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, PRIOR APPLICATION NUMBER: 60/092183
, PRIOR FILING DATE: 1998-07-09

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DB	61	TTTTGGGATTTTAATTTTCAACACACGACGAGATGACATTTTCTGTGCACATATATTATT	120	
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DB	121	GTTGGTATGTGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTCGGAGATGGCTA	180	
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DB	421	GTATCCCTCTCATATACAAATAAGGTGAATTTATAAGTACCTATGCGAGTTGGCTGGAC	480	
QY	481	AGTTCTAAATTTGGACHTTTTAAATTTTAAATTCAGTAACGTGATTTTATCACCTGGCTATGT	540	
DB	481	AGTTCTAAATTTGGACHTTTTAAATTTTAAATTCAGTAACGTGATTTTATCACCTGGCTATGT	540	
QY	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGGTCTCTCTCCCC	600	
DB	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGGTCTCTCTCCCC	600	
QY	601	TTACAGAATTGACATTTTAAATTCGGATACAGTTAGTAATAGGAATAATGACATTAGAAGG	660	
DB	601	TTACAGAATTGACATTTTAAATTCGGATACAGTTAGTAATAGGAATAATGACATTAGAAGG	660	

	AAGAATCACAGGAGAAAGGAACAAGGGAAAATAATTGTTCCTCCACAGCAAAAAA	713
QY	661 AAGAATCACAGGAGAAAGGAACAAGGGAAAATAATTGTTCCTCCACAGCAAAAAA	713
PB	661 AAGAATCACCAGGCGAACAGGGAAGAGGGGAAAAATGTTGCCACAGCAAAAAA	713

RESULT 14

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US-09-989-293A-376
; Sequence 376, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deencoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; APPLICANT: Zhong, Zhen
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   ACIDS Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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	Query Match	100.0%;	Score 713;	DB 9;	Length 713;
	Best Local	Similarity	100.0%;	Prod. No. 5e-161;	
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US-09-989-735-376

Sequence 376, Application US/09989735

Publication No. US20020193299A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary B.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989, 735
CURRENT FILING DATE: 2001-11-19
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GenCore version 5.1.6
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(without alignments)
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Searched: 682709 seqs, 277475446 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11	38.6	5.4	4526	2	US-08-308-887A-4
12	38.6	5.4	4526	3	US-08-881-094-4
13	38.4	5.4	58407	4	US-08-916-421B-2
14	38	5.3	19233	4	US-10-204-708-45
15	37.8	5.3	1537	4	US-09-626-959D-2
16	37.8	5.3	202001	4	US-09-734-674-3
17	37.6	5.3	1335	4	US-09-543-681A-1450
18	37.4	5.2	275	4	US-08-585-593A-42
19	37.4	5.2	361	3	US-09-018-584A-9
20	37.4	5.2	2422	1	US-07-867-106-5
21	37.4	5.2	5852	1	US-07-867-106-2
22	37.4	5.2	786431	4	US-09-751-389-3
23	37.2	5.2	832	4	US-09-621-976-2813
24	37.2	5.2	9064	4	US-08-961-527-17
25	37	5.2	2110	3	US-08-419-459-1
26	37	5.2	10160	4	US-09-097-319A-8
27	37	5.2	10323	4	US-09-280-428A-11

C 28	37	5.2	11784	4	US-09-097-319A-9	Sequence 9, Appl
C 29	37	5.2	11991	4	US-09-097-319A-10	Sequence 10, Appl
C 30	37	5.2	24595	6	5428147-1	Patent No. 5428147
C 31	36.8	5.2	10467	4	US-10-204-708-2	Sequence 2, Appl
C 32	36.8	5.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
C 33	36.6	5.1	10640	4	US-09-417-485D-5	Sequence 5, Appl
C 34	36.6	5.1	11131	4	US-10-204-708-27	Sequence 27, Appl
C 35	36.6	5.1	51952	3	US-08-947-823-1	Sequence 1, Appl
C 36	36.4	5.1	408	4	US-09-134-001C-1464	Sequence 1464, Ap
C 37	36.4	5.1	1946	4	US-09-886-319A-83	Sequence 83, Appl
C 38	36.4	5.1	3331	3	US-09-042-785A-1	Sequence 1, Appl
C 39	36.4	5.1	161652	4	US-09-497-855A-40	Sequence 40, Appl
C 40	36.2	5.1	6113	4	US-10-204-708-14	Sequence 14, Appl
C 41	36	5.0	6317	4	US-10-204-708-11	Sequence 11, Appl
C 42	36	5.0	11050	4	US-10-204-708-86	Sequence 86, Appl
C 43	36	5.0	50000	4	US-09-146-053-3	Sequence 3, Appl
C 44	35.8	5.0	1634	4	US-09-220-132-111	Sequence 111, App
C 45	35.8	5.0	2570	2	US-09-056-075-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-772-440-1
; Sequence 1, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 1966
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "Y = C or T"
US-08-772-440-1

Query March 10.9%; Score 77.6; DB 3; Length 2298;
Best Local Similarity 73.1%; Pred. No. 8.5e-11;
Matches 114; Conservative 0; Mismatches 39; Indels 3; Gaps 1;


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; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match
Best Local Similarity 6.3%; Score 45.2; DB 4; Length 832;
Matches 40; Conservative 108; Mismatches 81; Indels 1; Gaps 1;

QY 364 GATTCATGATCTGAATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTATGTA 423
Db 149 KAWTWWKTYTAAATRYWMCWTKRPMASWYCWNGKARKWSTWRKRSRYASARSA 208

QY 424 TCCTGTCTATATACATAAAGCTGAAATTTAAGTACCCTATGCGCTTGGCTGGACAGT 483
Db 209 KRCVSCSWGAMGSKYMWWRWGWATGAGKAWRASCMWRKYAGKSKTSYKSMWMCW 268

QY 484 T-CTAATTCGACTTTATTAATTTTAAATCAGTAACTGATTATCAGTGTATGTC 542
Db 269 TRSWKYCYTKARWTGYCYRKGGMWGRGWYASKYKMWKRWMCWARMYRSTGTASRM 328

QY 543 TTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGT 592
Db 329 WWRWYTYTMMKWKYAWARAAARWAWWAWRRACAAATATAATTT 378

RESULT 5
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIOYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match
Best Local Similarity 6.2%; Score 44; DB 4; Length 640681;
Matches 89; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 415 TGTAAATGATCCCTGTCATATACATAAGGTGAATTAATTAAGTACCCTATGCGAGTGG 474
Db 117509 TGTATGAATACCCCTGAAATTTCTAAATGTCGAAGTCAGACAAATAACTGTGTAATATG 117568

QY 475 CTGGACAGTCTTAAATGGACTTTATTAAATTTTAAATCAGTAACTGATTTATCACTGG 534
Db 117569 GTTAAATATGATATATGCTTTTAAATGAGTATATTTCTATAAGGATTTAATCTGT 117628

QY 535 CTATGTGCTTAGATCTCTACAGGAGATCATATAATTTTGATACAAAT 578

; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/920,672
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 5847
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-920-672-10

Query Match
Best Local Similarity 5.7%; Score 40.4; DB 4; Length 5847;
Matches 56; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 632 TTAGATAGAAATATGACATTAGAAAGGAAGGAATCAGAGGAGAAAGGAAGGAAGGAA 691
Db 1084 TTAGCTGGCGAATAGAAAAAAGAAAGAAAGAAAGGAGGAGGAGGAGGAGGAA 1143

QY 692 AATGTTGCCAAGGAAAAA 713
Db 1144 GCGAAGAAAGAAAGGAA 1165

RESULT 7
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1123..3123
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 3124..3297
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 3871..4072
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OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
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OTHER INFORMATION: 10-513-262 : polymorphic base C or T
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LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
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NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
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OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
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LOCATION: 8926
OTHER INFORMATION: 10-349-368 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12171
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12429
OTHER INFORMATION: 10-350-332 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13535

Query Match 5.6%; Score 39.6; DB 4; Length 20674;
Best Local Similarity 56.0%; Pred. No. 0.96;
Matches 75; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 464 TATGAGTTGGCTGGACAGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGA 523
Db 10371 TTTCAGATGTCCTCACATGTTCCATCGTGAGGTTTAAAGTTAAATGACTTAATGG 10430
QY 524 TTATCTACTGGCTATGTCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAG 583
Db 10431 TGTGACACAGCTAAATGCTACAAAAACATTAGTTCTTGCAAAATTTTTTTTTTCAGAG 10490
QY 584 AAAAGTGTCTCTC 597
Db 10491 ACAAGTCTCACTC 10504

RESULT 8
US-08-446-855A-1
Sequence 1, Application US/08446855A
Patent No. 5849573
GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
US-08-446-855A-1
Query Match 5.5%; Score 39.2; DB 2; Length 8920;
Best Local Similarity 46.6%; Pred. No. 0.95;
Matches 162; Conservative 0; Mismatches 183; Indels 3; Gaps 1;
QY 365 ATTCAATGATTGTAAATTTAAGGCAATAACACATATTAGTATTACCTTAGTGTAAATGAT 424
Db 418 ATACAATTATTAATATTTCATGTGTACACATTAAATATAGTTTACACTTCTTATAATAA 477
QY 425 CCCTGTCATATATACATTAAGGTGAATTTATATAGTACCTTATGAGTTGGCTGGACAGTT 484
Db 478 AACCATCTATATATATACACAAATATATATCTCCCAATATTGTGGTTCCTATAAAT 537
QY 485 CTAAATTTGGACTTTTATTAATTTTAAATCAGTAACCTGATTATCACTGGCTATGCTT 544
Db 538 TTATTTATATATTATTATTAATTTATTTATTTATTTATTTT---TTTCTTAGTTAT 594
QY 545 AGATCTACAGGAGATCATATAANTTTGATACAAATAAAGAAAGTGTCTCTCCCTTAC 604
Db 595 AAAATAGTAATCTACTTAATTTAAATAAAAAAAAAAAAAAAAAAAAAAGAAAAAAA 654
QY 605 AGAATTGACATTTTAATGCGATACAGTTAGATAGGAATATGACATTAGAAGGAAGA 664
Db 655 AAAATTTACATATGAAAAATGAACTTGATATATGTAATTTATATAATTTTAAACATAAA 714
QY 665 ATACAGGGGAGAAGGAAAGAGGAAATGTTGCCAAGGAAAAAAA 712
Db 715 TATAATGTATATAAAAAAAAAAGAAAAATGGGAAAAATATATATGA 762

RESULT 9
US-09-150-741-1
Sequence 1, Application US/09150741
Patent No. 6183996
GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
TITLE OF INVENTION: Synthetase II
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 8920
TYPE: DNA
ORGANISM: Plasmodium falciparum
US-09-150-741-1

Query Match 5.5%; Score 39.2; DB 3; Length 8920;
Best Local Similarity 46.6%; Pred. No. 0.95;
Matches 162; Conservative 0; Mismatches 183; Indels 3; Gaps 1;
QY 365 ATTCAATGATTGTAAATTTAAGGCAATAACACATATTAGTATTACCTTAGTGTAAATGAT 424
Db 418 ATACAATTATTAATATTTCATGTGTACACATTAAATATAGTTTACACTTCTTATAATAA 477
QY 425 CCCTGTCATATATACATTAAGGTGAATTTATATAGTACCTTATGAGTTGGCTGGACAGTT 484
Db 478 AACCATCTATATATATACACAAATATATATCTCCCAATATTGTGGTTCCTATAAAT 537

485	QY	CTAAATGGGACGCTTATTAATTTTAAAAATCAGTAAGTATTTTATCAGTGGGCTATGTGCTT	544
538	Db	TTATTTATATATTTATTTATTAATTTATTTCAATTTATTTATTTT...TTTCTTAGTTTAT	594
545	QY	AGATCTACAGGAGATCATATAATTTTGATACAAATAAAGAAAAGTGTTCTCTCCCTTAC	604
595	Db	AAAAATAGTAATCTACTAATTTTAAAAAAAATAAAAAAATAAAAAAAGAAAAA	654
605	QY	AGAAATTCACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGCATTTAGAAAGGAAGA	664
655	Db	AAATTTACATATGAAAATGAACTTGTTATATGTAAATTTATAAATATTTTAAACATAAA	714
665	QY	ATGACGGGAGAAAGGAAGGGAATGTTGCCAGGAAAAAAA	712
715	Db	TATAAATCTATAAAAAAATAAGAAAAATGGAATAAATAATATAGAA	762

RESULT 10

US-07-855-412B-4/c
; Sequence 4, Application US/07855412B

Patent No. 5378819
GENERAL INFORMATION:
APPLICANT: Ryan, C.A.; McGurl, B.F.; Pearce, G.L.
TITLE OF INVENTION: "SYSTEMIN"
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Troy
STATE: Michigan
COUNTRY: USA
ZIP: 48303

Query Match 5.4%; Score 38.6; DB 1; Length 4526;
Best Local Similarity 48.4%; Pred. No. 1.1;

Qy	371	TGATGTGTAATTTTAAAGCGAAATACACATATTAGTATTACCTTACTGTGTAATGTATCCCTGT	430
Db	2108	TGATGATATATTGGGATATATGTCCTTTTCAACAAATTTCTCTTTTACATATCCCTCCCT	2049
Qy	431	CATATATACAAATAAGGTGAAATTAATAGTACCCCTATGCAGTGTGGCTGGACAGTTTCTAAAT	490
Db	2048	GTAATATCCCTTTAATATAAATAATATTTCCACAGTCTAATTTTATTTATTCGTTTAAAC	1989
Qy	491	TGGACTTTATTAAATTTTTTAAATTCAGTAAACTGATTTATCACTGGCTATGTGCTTAGATCT	550

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RESULT 12
US-08-881-094-4/c
; Sequence 4, Application US/08881094A
; Patent No. 6022739
; GENERAL INFORMATION:
; APPLICANT: Ryan, Clarence A
; APPLICANT: Pearce, Gregory L
; APPLICANT: McGurk, Barry F
; TITLE OF INVENTION: Systemin
; FILE REFERENCE: 7555-000001CPB
; CURRENT APPLICATION NUMBER: US/08/881,094A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 08/308,887
; EARLIER FILING DATE: 1994-09-19
; EARLIER APPLICATION NUMBER: PCT/US93/02428
; EARLIER FILING DATE: 1993-03-18
; EARLIER APPLICATION NUMBER: 07/885,412
; EARLIER FILING DATE: 1992-03-19
; EARLIER APPLICATION NUMBER: 07/528,956
; EARLIER FILING DATE: 1990-05-25
; EARLIER APPLICATION NUMBER: PCT/US91/03685
; EARLIER FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 4526
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-08-881-094-4

Query Match          5.4%; Score 38.6; DB 3; Length 4526;
Best Local Similarity 48.4%; Pred. No. 1.1;
Matches 107; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 371 TGAATGTAATTTAAGCGAAATACACATATTAGTATACCTTAGTGTAAATGATCCCTGT 430
Db 2108 TGAATGTAATTTAAGCGAAATACACATATTAGTATACCTTAGTGTAAATGATCCCTGT 2049

QY 431 CATATATACAAATGAAGTGAATATATAGTACCTTAGTGTAAATGATCCCTTAGTGTAAAT 490
Db 2048 GTAATATACCTTTAATATATATATATATATATATATATATATATATATATATATATAT 1989

QY 491 TGAATGTAATTTAATTTTAAATCAGTAACTGATTTATCATCGCTATGCTTAGATCT 550
Db 1988 TGAACATATAAATTTTAAATTAATATATATATATATATATATATATATATATATATAT 1929

QY 551 ACAGGAGATCATATATATTTGATACAAATATAAGAAAGTGT 591
Db 1928 TTAAGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1888

RESULT 13
US-08-916-421B-2
; Sequence 2, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 58407
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (6485)..(6485)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-2

Query Match          5.4%; Score 38.4; DB 4; Length 58407;
Best Local Similarity 47.5%; Pred. No. 2.6;
Matches 114; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 346 TGTAAAGAAACACCTTAGATTCATGATGTAATTTAAGGCAATACACATATTAGTA 405
Db 700 TATGAAATATATCCCTTTCAACCAATTTAGATGTTATTAAGGAAAGCTCAAAATCAATT 759

QY 406 TTACCTTAGTGAATGTCATCCCTGTCATATACATATAGTGAATTTAAGTACCTTA 465
Db 760 AGATTTCTTTGAGAATATTTCAATAATATTTGAAAAAATTTGGTATTTTCAATAAGAT 819

QY 466 TGCAGTTGGCTGCACAGTTCTAAATTTGGACTTTATTAATTTTAAATCAGTAACGTGATT 525
Db 820 GGAAATATAGTCGTTATTAATGAGCATATTAATCAGTTCATCTCAATTAATATCATTT 879

QY 526 TATCACTGGCTATGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAGAA 585
Db 880 GAGAGTAGATAAAGTGTGTCATATACGTTTAGAAGCTCAATAGACTACTACATATAATAA 939

RESULT 14
US-10-204-708-45
; Sequence 45, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: FIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 45
; LENGTH: 19233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228).
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 04:03:10 ; Search time 462 Seconds
(without alignments)
6556.202 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aaataatcatctatttcatca.....tgttgccaaggaaaaaaa 713

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002s:*
- 7: Geneseq2003as:*
- 8: Geneseq2003bs:*
- 9: Geneseq2003cs:*
- 10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	713	100.0	713	3	Aaz65094 Membrane-
2	713	100.0	713	3	Aac58634 Human PRO
3	713	100.0	713	4	Aas21480 Human CDN
4	713	100.0	713	5	Aaf44240 Human PRO
5	713	100.0	713	7	Abx77952 Human PRO
6	713	100.0	713	7	Abx80364 Novel hum
7	713	100.0	713	7	Abx80364 Novel hum
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9	713	100.0	713	7	Abx80364 Novel hum
10	713	100.0	713	7	Abx80364 Novel hum
11	713	100.0	713	7	Abx80364 Novel hum
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ALIGNMENTS

RESULT 1

Aaz65094
ID AAZ65094 standard; cDNA; 713 BP.
XX
AC AAZ65094;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1159 encoding cDNA.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 05-JUN-1998; 98US-0088555P.
PR 09-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088723P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
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PR 10-JUN-1998; 98US-0088811P.

Aca68006 Novel hum
Aca88455 Human sec
Acd81962 cDNA enco
Ada45992 Novel hum
Ada76423 Human PRO
Ada19073 Human PRO
Ada61696 Homo sapi
Adb19481 Novel hum
Adb28022 cDNA enco
Ada86501 Novel hum
Adb16065 Human PRO
Ada37887 Human CDN
Ada47851 Human PRO
Ada21573 Human CDN
Ada10360 Human CDN
Ada67646 Human PRO
Adb30653 cDNA enco
Ada85949 Novel hum
Ada17904 cDNA enco
Ada97161 Human PRO
Ada79465 Human PRO
Ada87604 Novel hum

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PR 01-JUL-1998; 98US-0091358P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX
XX
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX
XX WPI: 2000-072883/06.
XX P-PSDB; AAY66748.
XX
XX Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 271; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
XX
XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 713; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATATCATCTATTATCATTAATCAATATGATGATTTTATTTATTCATTAACATTGGG 60
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Db 1 AATATATCACTATTTATCATTAATCAATAATGTAATCTTTATTCATTAACAATTTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAAAACACAGCAGAAATGACATTTTCTGTGCTACTATTAAT 120
Db 61 TTTTGGGATTTTAAATTTTCAAAACACAGCAGAAATGACATTTTCTGTGCTACTATTAAT 120
QY 121 GTTGGTATGTAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
Db 121 GTTGGTATGTAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
QY 181 CTTTCTATCAAGAAATAAAGAGAACCAACAGTCAACCCACCAATCATCTTTTGAAGACAG 240
Db 181 CTTTCTATCAAGAAATAAAGAGAACCAACAGTCAACCCACCAATCATCTTTTGAAGACAG 240
QY 241 TGTGACTCTTACCAAGCTGTCAAAACCAAGCAGGAGGATAGTTAAAGACGGAATCT 300
Db 241 TGTGACTCTTACCAAGCTGTCAAAACCAAGCAGGAGGATAGTTAAAGACGGAATCT 300
QY 301 TGAATCAAGAGGTTAAATCTTGTGCTGAAGCTGGGAGGCTGTAAGAAAAACAC 360
Db 301 TGAATCAAGAGGTTAAATCTTGTGCTGAAGCTGGGAGGCTGTAAGAAAAACAC 360
QY 361 TTAGATCAATGATTTAAATTTAAGGCAATATACATATTTAGTATTTACCTTAGTGTAA 420
Db 361 TTAGATCAATGATTTAAATTTAAGGCAATATACATATTTAGTATTTACCTTAGTGTAA 420
QY 421 GTATCCCTGTCATATACATTAAGTGAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 480
Db 421 GTATCCCTGTCATATACATTAAGTGAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 480
QY 481 AGTTCTAAATGGACTTTTAAATTTTAAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 540
Db 481 AGTTCTAAATGGACTTTTAAATTTTAAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 540
QY 541 GCTTAGATCTACAGGAGATCATATTAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 600
Db 541 GCTTAGATCTACAGGAGATCATATTAATTTAAGTGAATTTAAGTGAATTTAAGTGAAT 600
QY 601 TTACAGAAATTTGACATTTTAAATTTAAGTGAATTTAAGTGAATTTAAGTGAATTTAAG 660
Db 601 TTACAGAAATTTGACATTTTAAATTTAAGTGAATTTAAGTGAATTTAAGTGAATTTAAG 660
QY 661 AAGAAATCACAGGAGAAAGAAAGGAGAAATTTGTCAGGAGGAGGAGGAGGAGGAGGAG 713
Db 661 AAGAAATCACAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713

RESULT 2

AAC58634

ID AAC58634 standard; cDNA; 713 BP.

XX

AC AAC58634;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.

XX

KW Human; immune related disease; diagnosis; anti-inflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antiporiatric; antiallergic;
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease; ss.

XX

OS Homo sapiens.

XX

PN WC200053758-A2.

XX

PD 14-SEP-2000.

XX

PF 02-MAR-2000; 2000WO-US005841.

XX

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99US-0123618P.

PR 12-MAR-1999; 99US-0123957P.

PR 23-MAR-1999; 99US-0125775P.

PR 12-APR-1999; 99US-0128849P.

PR 20-APR-1999; 99WO-US008615.

PR 28-APR-1999; 99US-0131445P.

PR 04-MAY-1999; 99US-0132371P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 03-OCT-1999; 99WO-US023089.

PR 29-OCT-1999; 99US-0162506P.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031274.

PR 03-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

XX

(GETH) GENENTECH INC.

XX

XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX

XX

DR WPI; 2000-572271/53.

DR P-PSDB; AAB33469.

XX

XX

PT

PT

PT

XX

XX

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 23; Fig 111; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and

CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 3; Length 713;

Best Local Similarity 100.0%; Pred. No. 2.7e-155;

Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	181	CTTTCTATCAAGAAATTAAGAGAACACACAGTCACCAATCATCTTTTGAAGACAG	240
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Db	241	TGTGACTCTTACCAAGCTCTCAAAACACAGGAGGCGATAGTTAAAGGACGGATCT	300
QY	301	TGACTCAAGAGGGTTAATTTCTGGTCTGAAGCCTGGGCGAGGCTTAAGAAACAC	360
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Db	361	TTAGATTCATGATTTGAATTTTAAAGCAATACACATATAGTATTACCTTAGTGTAA	420
QY	421	GTATCCCTGTCATATACATTAAGTGAATTAAGTACCCCTATGACGTTGGCTGGAC	480
Db	421	GTATCCCTGTCATATACATTAAGTGAATTAAGTACCCCTATGACGTTGGCTGGAC	480
QY	481	AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAATCATCTGCTATGT	540
Db	481	AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAATCATCTGCTATGT	540
QY	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATTAAGAAAGTGTCTCTCCC	600
Db	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATTAAGAAAGTGTCTCTCCC	600
QY	601	TTACAGAAATGACATTTTAAATGCGATACAGTTAGAAATAGCAATAGCAATAGG	660
Db	601	TTACAGAAATGACATTTTAAATGCGATACAGTTAGAAATAGCAATAGCAATAGG	660
QY	661	AAGAAATGACAGGAGAAAGGAAAGGAAAGGAAATGTTGCCAAGGAAAGAAAA	713
Db	661	AAGAAATGACAGGAGAAAGGAAAGGAAAGGAAATGTTGCCAAGGAAAGAAAA	713

RESULT 3

AAS21480

ID AAS21480 standard; cDNA; 713 BP.

XX

AC AAS21480;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA sequence encoding for PRO159 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;

KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;

KW A-peptide; factor VIIa; gene therapy; ss.

XX Homo sapiens.

OS

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032678.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US004914.

XX 24-FEB-2000; 2000WO-US005004.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 10-MAR-2000; 2000WO-US006319.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-MAR-2000; 2000WO-US007377.

XX 21-MAR-2000; 2000WO-US007532.

XX 30-MAR-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 03-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 11-AUG-2000; 2000WO-US022031.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX

PA (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Deenoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

DR P-PSDB; AAU12408.

XX

PT Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing PRO

PT polypeptides, and detect the presence of mammalian tumors e.g. lung,

PT breast, prostate, cervical.

XX

PS Claim 3; Fig 473; 813pp; English.

XX

CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO

CC polypeptides. The PRO polypeptides are useful to detect other PRO

CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 4; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATATCATCTATTATCATTAATCAATTAATGTTATCTTTTATTCCTCAATTAACATTGGG 60
Db 1 AATATATCATCTATTATCATTAATCAATTAATGTTATCTTTTATTCCTCAATTAACATTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGTAATGACATTTTCTGTCACTATTATTATT 120
Db 61 TTTTGGGATTTTAAATTTTCAACACAGCAGTAATGACATTTTCTGTCACTATTATTATT 120
QY 121 GTTGTATGTGAGCTATTGTGAGATCCAAATTCAGGAACACACATTCGGGAATGGCTA 180
Db 121 GTTGTATGTGAGCTATTGTGAGATCCAAATTCAGGAACACACATTCGGGAATGGCTA 180
QY 181 CTTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAGACAG 240
Db 181 CTTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAGACAG 240
QY 241 TGTGACTCTACCAAGCTGTCAAAACACAGGAGGCGGTAGTAAAGCGGAATCT 300
Db 241 TGTGACTCTACCAAGCTGTCAAAACACAGGAGGCGGTAGTAAAGCGGAATCT 300
QY 301 TGACTCAAGAGGTTAAATCTTTGGTGTCTGAGCCTGGGCGAGGGGTAAAGAAAACAC 360
Db 301 TGACTCAAGAGGTTAAATCTTTGGTGTCTGAGCCTGGGCGAGGGGTAAAGAAAACAC 360
QY 361 TTGATTCATGATTTAAATTTAAAGGCAATACATATTAGTATTACCTTAGTGTAAAT 420
Db 361 TTGATTCATGATTTAAATTTAAAGGCAATACATATTAGTATTACCTTAGTGTAAAT 420
QY 421 GATCCCTGTCATATATCAATTAAGGTGAAATTAATAGTACCTTACGATGGCTGGAC 480
Db 421 GATCCCTGTCATATATCAATTAAGGTGAAATTAATAGTACCTTACGATGGCTGGAC 480
QY 481 AGTTCTAAATTCGACTTTTAAATTTTAAATTCAGTAACTATTCATCTGGCTATGT 540
Db 481 AGTTCTAAATTCGACTTTTAAATTTTAAATTCAGTAACTATTCATCTGGCTATGT 540
QY 541 GCTTAGATCTACAGGAGATCATATATTGATACAAATAAAGAAAGTGTCTCTCCCC 600
Db 541 GCTTAGATCTACAGGAGATCATATATTGATACAAATAAAGAAAGTGTCTCTCCCC 600
QY 601 TTACAGATTCGACTTTTAAATTCGATACATAGTATAGGAAATATGACATTAGAAGG 660
Db 601 TTACAGATTCGACTTTTAAATTCGATACATAGTATAGGAAATATGACATTAGAAGG 660
QY 661 AAGAATGACAGGAGAAAGAAAGGAAATGTTGCCAAGGAAAAAAA 713
Db 661 AAGAATGACAGGAGAAAGAAAGGAAATGTTGCCAAGGAAAAAAA 713

RESULT 4

AAAF44240
ID AAF44240 standard; cDNA; 713 BP.
XX
AC AAF44240;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay; ss.
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-01410372.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
(GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
PI Zhang Z;
XX
WPI; 2001-032160/04.
P-PSDB; AAB65271.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 2; Fig 271; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide

CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
 CC AAF65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match	100.0%;	Score 713;	DB 5;	Length 713;
Best Local Similarity	100.0%;	Pred. No. 2.7e-155;		
Matches 713;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	AATATATCATCTATTTATCATTAATCAATGAATGATCTCTTTTATTCCTAATAACATTTGGG	60
DB	1	AATATATCATCTATTTATCATTAATCAATGAATGATCTCTTTTATTCCTAATAACATTTGGG	60
QY	61	TTTTGGGATTTAAATTTCAACACAGCAGATGACATTTTCTGTCATTAATTAAT	120
DB	61	TTTTGGGATTTAAATTTCAACACAGCAGATGACATTTTCTGTCATTAATTAAT	120
QY	121	GTGTGATGTCGAGCTATTTGGAGATCCCAATTCAGGAACACACATTCGGAGATGGCTA	180
DB	121	GTGTGATGTCGAGCTATTTGGAGATCCCAATTCAGGAACACACATTCGGAGATGGCTA	180
QY	181	CTTCTTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAAGACAG	240
DB	181	CTTCTTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAAGACAG	240
QY	241	TGTGACTCTACAAAGCTGTCAAAACACAGCAGGCGGCTAGTTAAAGACGGAATCT	300
DB	241	TGTGACTCTCTACAAAGCTGTCAAAACACAGCAGGCGGCTAGTTAAAGACGGAATCT	300
QY	301	TGACTCAAGAGGTTAAATCTTGGTCTGAAGCTGGGCGAGGGGTAAAGAAAAACAC	360
DB	301	TGACTCAAGAGGTTAAATCTTGGTCTGAAGCTGGGCGAGGGGTAAAGAAAAACAC	360
QY	361	TTAGATTCATGATGTAATTTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420
DB	361	TTAGATTCATGATGTAATTTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420
QY	421	GTATCCCTCTCATATATACAAAGTGAAATTAAGTACCCATGACGATGGCTGGAC	480
DB	421	GTATCCCTCTCATATATACAAAGTGAAATTAAGTACCCATGACGATGGCTGGAC	480
QY	481	AGTTCTAAATGACATTTAATTTTAAATTCAGTAACTGATTTATCACTGGCTATCT	540
DB	481	AGTTCTAAATGACATTTAATTTTAAATTCAGTAACTGATTTATCACTGGCTATCT	540
QY	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCC	600
DB	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCC	600
QY	601	TTACAGAATTTGACATTTTAAATTCGATACAGTTAGAAATAGGAATATGACATTAGAAAG	660
DB	601	TTACAGAATTTGACATTTTAAATTCGATACAGTTAGAAATAGGAATATGACATTAGAAAG	660
QY	661	AGAATGACAGGAGAAAGAAAGAAAGAAATGTTGCCAGGAAAAA	713
DB	661	AGAATGACAGGAGAAAGAAAGAAAGAAATGTTGCCAGGAAAAA	713

RESULT 5
 ID ABX77952
 AC ABX77952 standard; cDNA; 713 BP.
 XX
 AC ABX77952;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human PRO polynucleotide #118.
 XX
 XX Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;

KW	liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW	antibody-dependent enzyme mediated prodru therapy.
XX	
OS	Homo sapiens.
XX	
PN	US2003027163-A1.
XX	
PD	06-FEB-2003.
XX	
PF	15-NOV-2001; 2001US-00997666.
XX	
PR	16-JUN-1997; 97US-0049787P.
PR	17-OCT-1997; 97US-0062250P.
PR	05-NOV-1997; 97WO-US020069.
PR	12-NOV-1997; 97US-0065186P.
PR	13-NOV-1997; 97US-0065311P.
PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
PR	20-MAR-1998; 98US-0078910P.
PR	28-APR-1998; 98US-0083322P.
PR	07-MAY-1998; 98US-0084600P.
PR	28-MAY-1998; 98US-0087106P.
PR	02-JUN-1998; 98US-0087607P.
PR	02-JUN-1998; 98US-0087609P.
PR	02-JUN-1998; 98US-0087759P.
PR	03-JUN-1998; 98US-0087827P.
PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088025P.
PR	04-JUN-1998; 98US-0088028P.
PR	04-JUN-1998; 98US-0088028P.
PR	04-JUN-1998; 98US-0088029P.
PR	04-JUN-1998; 98US-0088030P.
PR	04-JUN-1998; 98US-0088033P.
PR	04-JUN-1998; 98US-0088326P.
PR	05-JUN-1998; 98US-0088167P.
PR	05-JUN-1998; 98US-0088202P.
PR	05-JUN-1998; 98US-0088212P.
PR	05-JUN-1998; 98US-0088217P.
PR	09-JUN-1998; 98US-0088659P.
PR	10-JUN-1998; 98US-0088734P.
PR	10-JUN-1998; 98US-0088738P.
PR	10-JUN-1998; 98US-0088742P.
PR	10-JUN-1998; 98US-0088810P.
PR	10-JUN-1998; 98US-0088824P.
PR	10-JUN-1998; 98US-0088826P.
PR	11-JUN-1998; 98US-0088858P.
PR	11-JUN-1998; 98US-0088861P.
PR	11-JUN-1998; 98US-0088878P.
PR	12-JUN-1998; 98US-0089105P.
PR	16-JUN-1998; 98US-0089440P.
PR	16-JUN-1998; 98US-0089512P.
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PR	17-JUN-1998; 98US-0089653P.
PR	18-JUN-1998; 98US-0089801P.
PR	18-JUN-1998; 98US-0089907P.
PR	18-JUN-1998; 98US-0089908P.
PR	19-JUN-1998; 98US-0089947P.
PR	19-JUN-1998; 98US-0089948P.
PR	22-JUN-1998; 98US-0090246P.
PR	22-JUN-1998; 98US-0090252P.
PR	22-JUN-1998; 98US-0090254P.
PR	23-JUN-1998; 98US-0090349P.
PR	23-JUN-1998; 98US-0090355P.
PR	24-JUN-1998; 98US-0090429P.
PR	24-JUN-1998; 98US-0090431P.
PR	24-JUN-1998; 98US-0090435P.
PR	24-JUN-1998; 98US-0090444P.

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PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
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PR 26-JUN-1998; 98US-0090862P.
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PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
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PR 07-JUL-1998; 98US-0091978P.
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PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 19-AUG-1998; 98US-0097022P.
PR 20-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097978P.
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PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0090445P.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2,7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATATCATCTATTATTCATTAATCAATATGTAATCTTTTATTCATTAACATTTGGG 60
DB 1 AATATATCATCTATTATTCATTAATCAATATGTAATCTTTTATTCATTAACATTTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTAT 120
DB 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCTACTATTATTAT 120
QY 121 GTTGTATGTGAAGCTATTGGAGATCCAAATTCAGAAAGCAACATTTGGAGAAATGGCTA 180
DB 121 GTTGTATGTGAAGCTATTGGAGATCCAAATTCAGAAAGCAACATTTGGAGAAATGGCTA 180
QY 181 CTTTCTATCAAGAAATAAGAGAACCCACAGTCAACCCACACAAATCATCTTTAGAGACAG 240
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DB 301 TGACTCAAGAGGGTTAATCTTGTGTGAAGCCCTGGGCGCAGGGGTGTAAGAAAAACAC 360
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PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
PR (GETH ) GENENTECH INC.
PR
PR Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
PR Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PR Grimaldi JC, Gurney AL, Kljavan IJ, Napier MA, Pan J, Paoni NF;
PR Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PR Zhang Z;
PR
PR WFI; 2003-247083/24.
PR P-PSDB; ABUS9165.
PR
PR Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PR and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PR are therapeutically useful for enhancing immune response and in cancer
PR treatments.
PR
PR Claim 2; Fig 273; 648pp; English.
PR
PR The invention describes an isolated human PRO polypeptide. The PRO
PR polypeptides are useful in detecting PRO polypeptides in a sample, in
PR linking a bioactive molecule to a cell expressing a PRO polypeptide, and
PR in modulating at least one biological activity of a cell expressing a PRO
PR polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
PR useful for treating cardiac insufficiency disorders. PRO1154 and PRO1185
PR stimulate adrenal cortical capillary endothelial growth, and PRO336,
PR PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PR PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
PR useful for treating conditions or disorders where angiogenesis would be
PR beneficial, e.g. wound healing and antagonist of this polypeptide are
PR useful for treating cancerous tumours. PRO812 inhibits vascular
PR endothelial growth factor (VEGF) stimulated proliferation of endothelial
PR cells and is thus useful for inhibiting endothelial cell growth in
PR mammals which would be beneficial in inhibiting tumour growth. PRO826,
PR PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
PR stimulated T-lymphocytes and are therapeutically useful for enhancing
PR immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
PR retinal neurons cells (PRO1132 is also enhances survival/proliferation of
PR rod photoreceptor cells) and therefore are useful for treating retinal
PR disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
PR and PRO1066 induce proliferation of mammalian kidney mesangial cells,
PR and therefore are useful for treating kidney disorders associated with
PR decreased mesangial cell function such as Berger disease or other
PR nephropathies associated with dermatitis, herpeticiformis or Crohn's
PR disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
PR proliferation and/or redifferentiation of chondrocytes in culture and are
PR thus useful for treating sports injuries, and arthritis. This sequence
PR represents a novel human PRO protein polynucleotide
PR
PR Query Match
PR Best Local Similarity 100.0%; Score 713; DB 7; Length 713;
PR Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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PR 181 CTTTCTATCAAGAAATAAAGAGAACCAACAGTCAGTCAACCCACACATCATCTTTAGACAG 240
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RESULT 7

ACAG69270

ID ACA69270 standard; cDNA; 713 BP.

XX ACA69270;

XX 26-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1159.

Human; ss; gene; PRO; secreted protein; transmembrane protein;
cardiac insufficiency disorders; angiogenesis; wound healing;
cancerous tumour; immune response; retinal disorder; sight loss;
retinitis pigmentosa; age-related macular degeneration; AMD;
kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087108P.

XX 02-JUN-1998; 98US-0087607P.

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PR 31-AUG-1998; 98US-0098525P.
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PR 16-SEP-1998; 98US-0100634P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 07-OCT-1998; 98US-0101141P.
PR 01-DEC-1998; 98US-0113296P.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0113296P.
PR 08-MAR-1999; 98US-0123957P.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98US-0123957P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
PR 15-SEP-1999; 98US-0149396P.
PR 15-SEP-1999; 98US-0149396P.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98US-0158663P.
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PR 05-JAN-2000; 98US-0158663P.
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PR 11-FEB-2000; 98US-0158663P.
PR 18-FEB-2000; 98US-0158663P.
PR 18-FEB-2000; 98US-0158663P.

PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
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PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-341980/32.
DR P-PSDB; ABO17852.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 473; 660pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences

CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AATATATCATCTATTATCATTAATCAATATGATTTCTTTTATCCAAATACATTGGG 60
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RESULT 9
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ID ABX90341 standard; cDNA; 713 BP.
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AC ABX90341;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein cDNA, #154.
XX
KW Human; gene; sb; PRO; secreted; transmembrane; signal peptide;
XX pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
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PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napiet MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WL;
PI Zhang Z;

DR WPI; 2003-288106/28.
DR P-PSDB; ABU60595.

PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
XX Claim 2; Fig 271; 650pp; English.

CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or

CC natural sources. The sequences presented in ABX90083-ABX90468 are the
CC genes encoding, the primers amplifying and the probes detecting the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ

Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2,7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATATCATCTATTATCATCTAATTAATCAATATGATTTCTTTTATTCOAATAACATTTGGG 60
Db 1 AATATATCATCTATTATCATCTAATTAATCAATATGATTTCTTTTATTCOAATAACATTTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAACACACAGCAGAAATGACATTTTCTGTCACATATATTTAT 120
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QY 121 GTTGGTATGTAAGCTATTITGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
Db 121 GTTGGTATGTAAGCTATTITGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180
QY 181 CTTTCTATCAAGAAATTAAGAGAACACACAGTCAACCCACACATCATCTTTAGAAGACAG 240
Db 181 CTTTCTATCAAGAAATTAAGAGAACACACAGTCAACCCACACATCATCTTTAGAAGACAG 240
QY 241 TGTGACTCTTACCAAGCTCTGAAAACCCACAGCAGGCGATAGTTAAAGACGGAATCT 300
Db 241 TGTGACTCTTACCAAGCTCTGAAAACCCACAGCAGGCGATAGTTAAAGACGGAATCT 300
QY 301 TGACTCAAGAGGGTTAATCTTGGTGTGAAGCTGGGGCAGGGGTGTAAGAAAAAACAC 360
Db 301 TGACTCAAGAGGGTTAATCTTGGTGTGAAGCTGGGGCAGGGGTGTAAGAAAAAACAC 360
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Db 361 TTAGATTCATGATGTTAAATTTAAGCAATACACATATAGTATACCTTAGTGTAAAT 420
QY 421 GTATCCCTGTCTATATACATTAAGTGAATTTAATTAAGTACCTATGCACTTGGCTGGAC 480
Db 421 GTATCCCTGTCTATATACATTAAGTGAATTTAATTAAGTACCTATGCACTTGGCTGGAC 480
QY 481 AGTCTTAAATGGACTTTTAAATTTTAAATTCAGTAACTGATTTATCACTGGCTATGT 540
Db 481 AGTCTTAAATGGACTTTTAAATTTTAAATTCAGTAACTGATTTATCACTGGCTATGT 540
QY 541 GCTTAGATCTACAGGAGATCATATATTTTGAACAATTAAGTAACTGATTTATCACTGGCTATGT 600
Db 541 GCTTAGATCTACAGGAGATCATATATTTTGAACAATTAAGTAACTGATTTATCACTGGCTATGT 600
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Db 601 TTACAGAATTCAGATTTTAAATCCGATACAGTTAGAAATAGGAATATGACATTAGAAAG 660
QY 661 AAGAAATGACAGGAGAAAGAAAGAGGAAATGTGCCAGGAAAAA 713
Db 661 AAGAAATGACAGGAGAAAGAAAGAGGAAATGTGCCAGGAAAAA 713

RESULT 10

ABX64187

ID ABX64187 standard; cDNA; 713 BP.

XX

XX

AC

DT 26-FEB-2003 (first entry)

DE cDNA encoding human PRO159 polypeptide.

XX

XX

KW

KW

KW

KW

KW

KW

KW

gene therapy; gene; ss.
Homo sapiens.
US2002103125-A1.
01-AUG-2002.
20-NOV-2001; 2001US-00989731.
16-JUN-1997; 97US-00497787P.
17-OCT-1997; 97US-0062250P.
05-NOV-1997; 97WO-US020069.
12-NOV-1997; 97US-0065186P.
13-NOV-1997; 97US-0065531P.
24-NOV-1997; 97US-0066770P.
25-FEB-1998; 98US-0075945P.
20-MAR-1998; 98US-0078910P.
28-APR-1998; 98US-0083322P.
07-MAY-1998; 98US-0084500P.
28-MAY-1998; 98US-0087106P.
02-JUN-1998; 98US-0087607P.
02-JUN-1998; 98US-0087609P.
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03-JUN-1998; 98US-0087827P.
04-JUN-1998; 98US-0088021P.
04-JUN-1998; 98US-0088025P.
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04-JUN-1998; 98US-0088030P.
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05-JUN-1998; 98US-0088167P.
05-JUN-1998; 98US-0088202P.
05-JUN-1998; 98US-0088212P.
05-JUN-1998; 98US-0088217P.
09-JUN-1998; 98US-0088655P.
10-JUN-1998; 98US-0088734P.
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10-JUN-1998; 98US-0088742P.
10-JUN-1998; 98US-0088810P.
10-JUN-1998; 98US-0088824P.
10-JUN-1998; 98US-0088826P.
11-JUN-1998; 98US-0088858P.
11-JUN-1998; 98US-0088861P.
11-JUN-1998; 98US-0088876P.
12-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.
16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089598P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
17-JUN-1998; 98US-0089653P.
18-JUN-1998; 98US-0089801P.
18-JUN-1998; 98US-0089907P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX

(GETH) GENENTECH LTD.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Giersten ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavlin ID, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart FA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2003-102117/09.
 DR P-PSDB; ABU13977.
 DR

PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 PT

PS Claim 2; Fig 271; 649pp; English.

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for for
 CC identifying agonists or antagonists. The polynucleotide sequences
 CC encoding PRO polypeptides are useful as hybridisation probes, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC in the preparation of PRO polypeptides, for generating transgenic animals
 CC or knockout animals, to construct hybridisation probes for mapping the
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, for chromosome
 CC identification, as chromosome markers, and for generating probes for PCR,
 CC Northern analysis, Southern analysis, and Western analysis. The present
 CC sequence encodes a human PRO polypeptide of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/psipsdIDEntry.html
 XX

XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 7; Length 713;
 Best Local Similarity 100.0%; Pred. No. 2.7e-155;
 Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATATCATCTATTTATCATTAATCAATAATGTATTTCTTTATTTCAATAACATTTGGG 60
 DB 1 AATATATCATCTATTTATCATTAATCAATAATGTATTTCTTTATTTCAATAACATTTGGG 60
 QY 61 TTTTGGGATTTTAAATTTTCAAAACACAGCAGAGATGACATTTTCTGTCTACTATTATTATT 120
 DB 61 TTTTGGGATTTTAAATTTTCAAAACACAGCAGAGATGACATTTTCTGTCTACTATTATTATT 120
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 QY 241 TGTGACTCCTACCAAGCTGTCAAAACCCACAGCAGGCGCATAGTTAAAGGACGGGAATCT 300
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 QY 361 TTAGATTCAATGATTTGTAATTTAAGGCAATACACATATTAGTATTACCTTAGTCTAAT 420
 DB 361 TTAGATTCAATGATTTGTAATTTAAGGCAATACACATATTAGTATTACCTTAGTCTAAT 420
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 DB 481 AGTCTCTAAATTCGACTTTATTTTAAATTCAGTAATCATTTATCATCTGGCTATGT 540
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 QY 661 AAGAATGACAGGAGAGAAAGGAAAGGAAATGTTGCCAAGGAAAAA 713
 DB 661 AAGAATGACAGGAGAGAAAGGAAAGGAAATGTTGCCAAGGAAAAA 713

RESULT 11

ACA67230

ID ACA67230 standard; cDNA; 713 BP.

XX ACA67230;

AC ACA67230;

XX 23-JUN-2003 (first entry)

DT cDNA encoding human PRO polypeptide #237.

DE Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;

XX bone disorder; cartilage disorder; rheumatoid arthritis; obesity;

XX sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;

XX hearing loss; coagulation disorder; stroke; heart attack; cardiac;

XX antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;

XX antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.

XX Homo sapiens.

OS Homo sapiens.

XX US2003004311-A1.

PN 02-JAN-2003.

XX

XX

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PF 19-DEC-2001; 2001US-00028072.
XX
PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059358P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062846P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 28-OCT-1997; 97US-0063704P.
PR 28-OCT-1997; 97US-0063733P.
PR 28-OCT-1997; 97US-0063735P.
PR 03-NOV-1997; 97US-0063738P.
PR 07-NOV-1997; 97US-0064248P.
PR 12-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 21-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 11-DEC-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 01-DEC-1998; 98WO-US024855.
PR 05-JAN-1999; 98WO-US025108.
PR 08-MAR-1999; 98WO-US000106.
PR 10-MAR-1999; 98WO-US005028.
PR 20-APR-1999; 98WO-US005190.
PR 14-MAY-1999; 98WO-US008615.
PR 02-JUN-1999; 98WO-US010733.
PR 01-SEP-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.

108-SEP-1999; 99WO-US020594.
13-SEP-1999; 99WO-US020944.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
05-OCT-1999; 99WO-US023089.
29-NOV-1999; 99WO-US028214.
30-NOV-1999; 99WO-US028313.
30-NOV-1999; 99WO-US028409.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
02-DEC-1999; 99WO-US028551.
02-DEC-1999; 99WO-US028564.
16-DEC-1999; 99WO-US028565.
20-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
30-DEC-1999; 99WO-US030999.
30-DEC-1999; 99WO-US031243.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004342.
24-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
01-MAR-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005501.
XX
XX
(GETH ) GENENTECH INC.
XX
XX
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen MB, Goddard A, Godowski PU, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX
WPI; 2003-352836/33.
P-PSDB; ABU81106.
XX
XX
New isolated PRO polypeptide useful for treating diabetes, rheumatoid
arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
heart attack.
XX
XX
Claim 2; Fig 473; 643pp; English.
XX
XX
The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a medicament
useful in the treatment of diabetes, bone and/or cartilage disorders
(e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
(e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
assays for PRO, by detecting its expression in specific cells, tissues or
serum, and for affinity purification of PRO from recombinant cell culture
or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
the human PRO polypeptides of the invention. Note: The sequence data for
this patent was obtained in electronic format directly from the USPTO web
site at seqdata.uspto.gov/psipsdIDentry.html
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATATCATCTATTATCAATTAATCAATTAATGTTATCTTTTATTCCAATACATTGGG 60
Dd 1 AATATATCATCTATTATCAATTAATCAATTAATGTTATCTTTTATTCCAATACATTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAGATGACATTTTCTGTCACTATTATT 120
Dd 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAGATGACATTTTCTGTCACTATTATT 120

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QY 181 CTTTCTATCAAGAAATAAGAGAACCAACACAGTCAACCCACACAATCATCTTTTGAAGACAG 240
Db |||||
QY 181 CTTTCTATCAAGAAATAAGAGAACCAACACAGTCAACCCACACAATCATCTTTTGAAGACAG 240
Db |||||
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Db |||||
QY 241 TGTGACTCCCTACCAAGCTCTCAAAACCAAGCAAGGCGATAGTTAAAGGACGGAATCT 300
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Db |||||
QY 421 GTATCCCTGTATATATCAATTAAGTGAATTTAAATTCAGTAACTGATTTATCACTGGCTATGT 540
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QY 601 TTACAGATTTGACATTTTAAATTCAGTAACTGATTTATCACTGGCTATGT 660
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Db |||||
QY 661 AAGAATGACAGGAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 713
Db |||||
RESULT 12
ID ACA64409 standard; cDNA; 713 BP.
XX
XX ACA64409;
XX
XX 17-JUN-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO1159 cDNA.
XX
XX Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2003003531-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 19-NOV-2001; 2001US-00989734.
XX
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078310P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088032P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089588P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 02-JUN-1999; 99WO-US005028.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.


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PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US011252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006684.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854280.
PR 10-MAY-2001; 2001US-00860216.
PR 18-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.

PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
XX P-PSDB; ABU66806.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
XX Claim 2; Fig 473; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATATCATCTATTATCAATTAATCAATATGTAATCTTTTATTTCCAAATACATTGGG 60
DB 1 AATATATCATCTATTATCAATTAATCAATATGTAATCTTTTATTTCCAAATACATTGGG 60
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGATGATGATTTTCTGTCTACTATTATT 120
DB 61 TTTTGGGATTTTAAATTTTCAACACAGCAGATGATGATTTTCTGTCTACTATTATT 120
QY 121 GTTGTATGTGAAGCTATTTTGGAGATCCAATTCAGGAAGCAACACATTGGAGATGGCTA 180
DB 121 GTTGTATGTGAAGCTATTTTGGAGATCCAATTCAGGAAGCAACACATTGGAGATGGCTA 180
QY 181 CTTTCTATCAGAAATTAAGAACACAGTCAGTCAACCCACACATCATCTTTAGAGACAG 240
DB 181 CTTTCTATCAGAAATTAAGAACACAGTCAGTCAACCCACACATCATCTTTAGAGACAG 240
QY 241 TGTGACTCTCTACAAAGCTGTCAAAACACACAGCAGGAGGTCATAGTTAAAGGACGAATCT 300
DB 241 TGTGACTCTCTACAAAGCTGTCAAAACACACAGGAGGTCATAGTTAAAGGACGAATCT 300
QY 301 TGAATCAAGAGGGTTAATTTCTTGGTGTGAAGCCCTGGGCGGGGTGTAAAGAAAAACAC 360
DB 301 TGAATCAAGAGGGTTAATTTCTTGGTGTGAAGCCCTGGGCGGGGTGTAAAGAAAAACAC 360
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Db 301 TGACTCAAGAGGGTTAAATCTTGCTGCTGAAGCTGGGCGAGGGTGTAAAGAAAAACAC 360
Qy 361 TTAGATTCATGATGTTAAATTTAAGCAATACACATATAGTATACCTTAGTGTAT 420
Db 361 TTAGATTCATGATGTTAAATTTAAGCAATACACATATAGTATACCTTAGTGTAT 420
Qy 421 GTATCCCTGTCATATACAAATAAGGTGAATTTAAGTACCCTATGCAAGTTGGCTGGAC 480
Db 421 GTATCCCTGTCATATACAAATAAGGTGAATTTAAGTACCCTATGCAAGTTGGCTGGAC 480
Qy 481 AGTTCTAAATGACATTTATTAATTTTAAATTCAGTAATGATTTATACCTGGCTATGT 540
Db 481 AGTTCTAAATGACATTTATTAATTTTAAATTCAGTAATGATTTATACCTGGCTATGT 540
Qy 541 GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAGGAGGAGTCTCTCCCC 600
Db 541 GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAGGAGGAGTCTCTCCCC 600
Qy 601 TTACAGAAATGACATTTTAAATGCGATACAGTTAGAAATAGCAATATGACATTAGAAAG 660
Db 601 TTACAGAAATGACATTTTAAATGCGATACAGTTAGAAATAGCAATATGACATTAGAAAG 660
Qy 661 AAGAAATCAGAGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713
Db 661 AAGAAATCAGAGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713

RESULT 14
ABX89377
ID ABX89377 standard; cDNA; 713 BP.
AC
XX
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO1159.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PE 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021441.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030352.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808589.
PR 22-MAR-2001; 2001US-00816744.
PR 03-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
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21-JUN-2001; 2001US-00887879.
 22-JUN-2001; 2001WO-US020116.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 18-JUL-2001; 2001US-00908827.
 06-AUG-2001; 2001US-00924419.
 09-AUG-2001; 2001US-00927796.
 16-AUG-2001; 2001US-00931836.
 19-DEC-2001; 2001US-00028072.
 (GETH) GENENTECH INC.
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI; 2003-148238/14.
 P-PSDB; ABUS9897.
 Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
 Claim 2; Fig 473; 659pp; English.
 The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumors. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence encodes a novel human PRO protein

181 CTTTCTATCAAGAAATAAGAGAACCACTCAACCCACACCAATCATCTTTAGAGACAG 240
 181 CTTTCTATCAAGAAATAAGAGAACCACTCAACCCACACCAATCATCTTTAGAGACAG 240
 241 TGTGACTCTTCAAAAGCTGTCAAAACCAAGGAGGGGATGTTAAAGACGGAATCT 300
 241 TGTGACTCTTCAAAAGCTGTCAAAACCAAGGAGGGGATGTTAAAGACGGAATCT 300
 301 TGTGACTCAAGAGGGTAAATCTTGGTGTGAAGCTGGGCGAGGGTCTAAAGAAAAACAC 360
 301 TGTGACTCAAGAGGGTAAATCTTGGTGTGAAGCTGGGCGAGGGTCTAAAGAAAAACAC 360
 361 TTGAGTTCATGATGTTAAATTTAAAGGCAATACACATATTAGTATTACCTTAGTGTAA 420
 361 TTGAGTTCATGATGTTAAATTTAAAGGCAATACACATATTAGTATTACCTTAGTGTAA 420
 421 GTATCCCTGTCTATATACAAATTAAGTGAATATTAAGTACCTTATGCGTGGCTGGAC 480
 421 GTATCCCTGTCTATATACAAATTAAGTGAATATTAAGTACCTTATGCGTGGCTGGAC 480
 481 AGTTCTAAATGGACCTTTATTTTAAATCAAGTAACTGATTTATCACTGGCTATGT 540
 481 AGTTCTAAATGGACCTTTATTTTAAATCAAGTAACTGATTTATCACTGGCTATGT 540
 541 GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAAAAAGTGTCTCTCCC 600
 541 GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAAAAAGTGTCTCTCCC 600
 601 TTACAGAAATGACATTTTAAATGGATACAGTTAGAAATAGGAATATGACATTAGAAAG 660
 601 TTACAGAAATGACATTTTAAATGGATACAGTTAGAAATAGGAATATGACATTAGAAAG 660
 661 AAGAATCACAGGAGAAAGGAAGGAAAGGAAATTTTCCCAAGGAAAAA 713
 661 AAGAATCACAGGAGAAAGGAAGGAAAGGAAATTTTCCCAAGGAAAAA 713
 RESULT 15
 ABX80868
 ID ABX80868 standard; cDNA; 713 BP.
 AC ABX80868;
 XX
 DT 22-APR-2003 (first entry)
 DE Human secreted/transmembrane protein cDNA, #154.
 KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
 KW tumour-associated antigenic target; TAT; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
 OS Homo sapiens.
 FN US2003027162-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 15-NOV-2001; 2001US-00997428.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
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PR 11-FEB-2000; 2000WO-US003565.
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 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
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Query Match 100.0%; Score 713; DB 7; Length 713;

Best Local Similarity 100.0%; Pred. No. 2.7e-155;

Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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PAT 20-DEC-2002

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REFERENCE Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
AUTHORS Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kijavini, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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Genentech Inc. (US)
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REFERENCE Baker, K.P., Beresini, M., Defoige, L., Desnovers, L., Filivato, E.,
AUTHORS Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;
Genentech Inc. (US)
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DEFINITION Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.
ACCESSION AY358685
VERSION AY358685.1 GI:37182491
KEYWORDS FLI CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
AUTHORS Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B.,
Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E.,
Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S.,
Lee J., Lewis L., Liao L., Mark M., Robbie E., Sanchez C.,
Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V.,
Stinson J., Vagts A., Vandlen R., Watanabe C., Wiand D., Woods K.,
Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,
Goddard W.I. and Godowski P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 713)
REFERENCE Clark H.F.
AUTHORS Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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source 1. 713
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Best Local Similarity 100.0%; Pred. No. 7.3e-136;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CTTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACAATCATCTTTAGAGACAG 240
Db 181 CTTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACAATCATCTTTAGAGACAG 240
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Db 301 TGACTCAAGAGGGTTAAATTTCTTGGTGTGAAGCCCTGGGGGAGGGGTGTAAAGAAAAAACAC 360
QY 361 TTAGATTCAATGATTGTAAATTTTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAA 420
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QY 481 AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGATTTATCTACCTGCTATGT 540
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QY 541 GCTTAGATCTACAGGAGATCATATATTTGATACAAATAAAGAAAGTGTCTCTCCCC 600
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RESULT 6
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LOCUS Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute
DEFINITION Human BAC Library) complete sequence.
ACCESSION AC024224
VERSION AC024224.33 GI:21240476
KEYWORDS HTG
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 165414)
AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C.,
Alsbrooks S.L., Amaratunga H.C., Are J.R., Ayele M., Banks T.,
Barbieri J., Benton J., Binage K., Blankenburg K., Bonnin D.,
Bouck J., Bowe S., Brieva M., Brown E., Brown M., Bryant N.P.,
Buhay C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
Carroll T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,
Chen G., Chen R., Chen Z., Chiu D., Chowdhry I., Christopoulos C.,
Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H.,
Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
Earhart C., Edgar D., Edwards C.C., Elhaj N., Emerling S.,
Escotto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P.,
Frantz P., Gabisi A., Gao J., Garcia A., Garner T., Garza N.,
Gill R., Gorrell J.H., Guevara W., Gunaratne P., Hale S.,
Hamilton K., Han J., Harris C., Harris K., Hart M., Havlak P.,
Hawes A., Hernandez J., Hernandez O., Hodgson A., Hogues M.,
Holloway C., Hollins B., Homsi F., Howard S., Huber J., Hulyk S.,
Hume J., Ioshikhes I., Jackson L.E., Jacobson B., Jia Y.,
Johnson R., Jolivet S., Joudah S., Karlsson E., Kelly S., Khan U.,
King L., Korvah J., Kovar C., Kratovic J., Kureshi A., Landry N.,
Leal B., Lee E., Lewis L., Lewis L., Li J., Li Z., Lichtarge O.,
Lieu C., Liu J., Liu W., Loulseged H., Lozado R.J., Lu X.,
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Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Fu, J.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoohtari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstein, G. and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base

quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES

Location/Qualifiers

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repeat_region

repeat_region

misc_feature

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/function="unresolved homopolymeric run"

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Matches 708; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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AC006510/c

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DEFINITION

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AC006510 240864 bp DNA linear HTG 14-SEP-2000
Homo sapiens clone RP11-13C13, RP11-656E20, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.

AC006510 AC006514

AC006510.8 GI:10122018

HTG: HTGS PHASE1.

Source Homo sapiens (human)

Organism Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 240864)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Albrooks, S.L., Amarantunga, H.C., Are, J.R., Banks, T., Barbaccia, J.,
Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowles, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgatz, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, K., Harris, K., Hart, M., Havlak, P., Hawes, A.,
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Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulsegh, H., Lora, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, N., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, Z., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, A., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
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Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
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Watkinson, S., Williams, G., Williamson, A., Wlezyk, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 240864)

Worley, K.C.

Direct Submission

REFERENCE

AUTHORS

JOURNAL

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: J-33
Center clone name: RP11-13C13, RP11-656E20
Sequencing vector: Plasmid; M7789
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 77% of reads

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: J-33
Center clone name: RP11-13C13, RP11-656E20
Sequencing vector: Plasmid; M7789
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 77% of reads

Chemistry: Dye-terminator Big Dye: 23% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71594 bases at least Q40
Consensus quality: 93014 bases at least Q30
Consensus quality: 110702 bases at least Q20
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Estimated insert size: 331000; agarose-fp estimation
Quality coverage: 0.6x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 111085: contig of 111085 bp in length
* 111086 11185: gap of unknown length
* 11186 134782: contig of 23597 bp in length
* 134783 134882: gap of unknown length
* 134883 163654: contig of 28772 bp in length
* 163655 163754: gap of unknown length
* 163755 185050: contig of 21296 bp in length
* 185051 185350: gap of unknown length
* 185351 194802: contig of 9652 bp in length
* 194803 194903: gap of unknown length
* 194904 202527: contig of 7625 bp in length
* 202528 202628: gap of unknown length
* 202629 208558: contig of 6031 bp in length
* 208559 208759: gap of unknown length
* 208760 221786: contig of 13027 bp in length
* 221787 230142: contig of 8257 bp in length
* 230143 230242: gap of unknown length
* 230243 232625: contig of 2383 bp in length
* 232626 232725: gap of unknown length
* 232726 234559: contig of 1734 bp in length
* 234560 235821: contig of 1262 bp in length
* 235822 235921: gap of unknown length
* 235922 237146: contig of 1225 bp in length
* 237147 237246: gap of unknown length
* 237247 238417: contig of 1171 bp in length
* 238418 238517: gap of unknown length
* 238518 239649: contig of 1132 bp in length
* 239650 239750: gap of unknown length
* 239751 240864: contig of 1115 bp in length.

FEATURES
Source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-13C13, RP11-656B20"

ORIGIN

Query Match 82.8%; Score 590.2; DB 2; Length 240864;
Best Local Similarity 96.2%; Pred. No. 3.9e-111;
Matches 690; Conservative 0; Mismatches 18; Indels 9; Gaps 8;
QY 1 AATATATCATCTATTATCAATTAATCAATGATGATTTCTTTTCAATAAATTTG-G 59
Db 211751 ATTATATCATCTATTATCAATTAATCAATTTTGTATTTCTTTTCAATATCATTTGTG 211692
QY 60 GTTTTGGGATTTTAAATTTCAACACAGCAGATGACATTTTCTGCTACTATTTAT 119
Db 211691 GTTTTGGATTTTAAATTTCAACACAGCAGATGACATTTTCTGCTACTATTTAT 211632
QY 120 TGTGGTATGTGAAGCTATTGGAGATCCCAATTCAGGAGCAACACATTGGAGATGGCT 179

Db 211631 TGTGGTATGTGAAGCTATTGGAGATCCCAATTCAGGAGCAACACATTGGAGATGGCT 211572
QY 180 ACTTTC-TATCAAGAAATAAGAGAACACACAGT-CAACCCACACATCATCTTTAGAAGA 237
Db 211571 ACTTTC-TATCAAGAAATAAGAGAACACACAGTCCACCCACACATCTTCTTTAGAAGA 211512
QY 238 CAGTGTGACTCTCTACC-AAAGCTGTCAAAACCA-CAGGCAAGGGCATAGTTAA-AGGAGC 294
Db 211511 CAGTGTGACTCTCTACC-AAAGCTGTCAAAACCA-CAGGCAAGGGCATAGTTAA-CAGGAGC 211452
QY 295 GAATCTTGACTC-AAGAGGGTTAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGAAGA 353
Db 211451 GAATCTTGACTC-AAGAGGGTTAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGAAGA 211392
QY 354 AAAACACATTAGATTCATTAATGTTAAATTAAGGCAATATACATATTAGTATTACCTTA 413
Db 211391 AAAACACATTAGATTCATTAATGTTAAATTAAGGCAATATACATATTAGTATTACCTTA 211332
QY 414 GTGTAATGTATCCCTGTCTATATACATAAAGGTGAAATTAAGTACCCTATGCAATTG 473
Db 211331 GTGTAATGTATCCCTGTCTATATACATAAAGGTGAAATTAAGTACCCTATGCAATTG 211272
QY 474 GCTGACAGTCTTAATTTGGACTTTTAAATTTTAAATCAGTAACTGATTATCCTG 533
Db 211271 GCTGACAGTCTTAATTTGGACTTTTAAATTTTAAATCAGTAACTGATTATCCTG 211212
QY 534 GCTATGTCTTAGATCTCAGGAGATCATATAATTTGATACAAATATAAGGAAAAAGTTTC 593
Db 211211 GCTATGTCTTAGATCTCAGGAGATCATATAATTTGATACAAATATAAGGAAAAAGTTTC 211152
QY 594 TCT--CCCTTACAGAATTGACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGACA 651
Db 211151 TCTGCGCTTACACGAATTGACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGACA 211092
QY 652 TTAGAAAGGAAGATGACAGGAGAGAAAGGAAAGAGGGAATTTGTCACAGGAAAA 708
Db 211091 TTAGAAAGGAAGATGACAGGAGAGAGAAAGGAAAGAGGGAATTTGTCACAGGAAAA 211035

RESULT 8
AC138620/c
LOCUS
DEFINITION
Mus musculus chromosome UNK clone RP23-250E1, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
AC138620
AC138620.2 GI:28557995
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
Mus musculus
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 221471)
McPherson,J.D. and Waterston,R.H.
AUTHORS
The sequence of Mus musculus clone
TITLE
Unpublished
REFERENCE
2 (bases 1 to 221471)
McPherson,J.D. and Waterston,R.H.
AUTHORS
Direct Submission
TITLE
Submitted (12-JAN-2003) Genome Sequencing Center, 4444 Forest Park
JOURNAL
Parkway, St. Louis, MO 63108, USA
REFERENCE
3 (bases 1 to 221471)
McPherson,J.D. and Waterston,R.H.
AUTHORS
Direct Submission
TITLE
Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park
JOURNAL
Parkway, St. Louis, MO 63108, USA
COMMENT
On Feb 25, 2003 this sequence version replaced gi:27657609.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@wustl.edu
----- Project Information -----

Center project name: M_BA0250E01

Summary Statistics

Sequencing vector: M13; 0%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217739 bases at least Q40
Consensus quality: 218068 bases at least Q30
Consensus quality: 218373 bases at least Q20
Insert size: 193000; agarose-fp
Insert size: 227132; sum-of-contigs
Quality coverage: 14.88 in Q20 bases; agarose-fp
Quality coverage: 12.33 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1509: contig of 1509 bp in length
* 1510 1609: gap of unknown length
* 1610 3423: contig of 1814 bp in length
* 3424 3523: gap of unknown length
* 3524 8473: contig of 4950 bp in length
* 8474 8573: gap of unknown length
* 8574 13990: contig of 5417 bp in length
* 13991 14090: gap of unknown length
* 14091 20220: contig of 6130 bp in length
* 20221 20320: gap of unknown length
* 20321 33395: contig of 13075 bp in length
* 33396 33495: gap of unknown length
* 33496 46731: contig of 13236 bp in length
* 46732 46832: gap of unknown length
* 46832 62519: contig of 15687 bp in length
* 62519 80892: gap of unknown length
* 80893 103312: contig of 18274 bp in length
* 103313 103413: contig of 22320 bp in length
* 103413 125915: contig of 22502 bp in length
* 125915 171459: gap of unknown length
* 171459 171559: contig of 45445 bp in length
* 171460 221471: contig of unknown length
* 171560 221471: contig of 49912 bp in length.

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-250E1"
1..1509
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1610..3423
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3524..8473
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8574..13990
/note="assembly_name:Contig23"
14091..20220
/note="assembly_name:Contig24"
20321..33395
/note="assembly_name:Contig25"
33496..46731
/note="assembly_name:Contig26"
46832..62519
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62619..80892

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80993..103312
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misc_feature
103413..125914
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misc_feature
126015..171459
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/note="assembly_name:Contig31"
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171560..221471
/note="assembly_name:Contig32"

ORIGIN

Query Match 26.1%; Score 186; DB 2; Length 221471;
Best Local Similarity 63.2%; Pred. No. 1.7e-28;
Matches 456; Conservative 0; Mismatches 215; Indels 51; Gaps 9;
QY 1 AATATATCATCTATTATTCATTAATCAATAATGATTCT-TTATTCCAAATAACATTTGG 59
Db 87112 AACATACAGTTTATTATCAATAACCATAGGCATCCCTATATATGTCTCAATAATATGA 87053
QY 60 GTTTTGGGATTTTAAATTTTCAACACACAGCAGAAATGACAT--TTTTCCTGTCACTATTAT 117
Db 87052 GTGCTGGCATTTCCATTTTAAACACACAGCAGAAATGACATTTCTTTTCTGTCACTATTGT 86993
QY 118 ATTGTTGTATGTGAAGCTATTGAGATCCAAATTCAGAAACACACATTTGGAGAAATGG 177
Db 86992 GTTCGTGACGTATGAAGCATTTTGGTGACAAATTCAGGGAGAAATCCAGAGGAGAAAGA 86933
QY 178 CTACTTTCTATCAAGAAATAAGAGAACACACAGTCACCCACACATCATCTTTAGAAGA 237
Db 86932 CAATTCCTATCAAGAAATAAGAGAACACAC--AGCCACAGAAATCATCTTTAGATGA 86876
QY 238 CAGTGTGACTCTACCAAGCTGTCAAAACCAACAGCAAGGCAATGTTAAAGGA----- 292
Db 86875 GAAAGTGGCTCCTCCAGGCATCCAAACTACAGCAAGGCGACGCAAGAGGCAAT 86816
QY 293 CGGAATCTTGACTCAAGAGGGTTAATCTTGTGTGTAAGCTGGGCGAGGGGTGAAG 352
Db 86815 GGGATCCGGATTCAGAGGGTTCAATTCCTGTGTGAGGCTGGGGTGGGG----- 86764
QY 353 AAAACACATTAGATTCATGATTTGTAATTTAAAGGCAATAACACATATTAGTATTACCTT 412
Db 86763 -AATATGTTTACATCTATCAAGTGAATTCAGGCGACGACCTAACAGAAATCCCTT 86705
QY 413 AGTGAATCTATCCCTGTGCATATATACAAATAGGTGAATTAAGTACCCTATGAGTT 472
Db 86704 AGCATAACATA-CCCTGCCACAGACAGCTGTGTAAGTGGCATCAAAATCCACAGCTC- 86650
QY 473 GGCCTGACAGTTCATAATTTGGACTTTTAAATTTTAAATCAGTAACTGAT-TTATCAC 531
Db 86649 -----TTTCACCTTAAAGGAGCGATTAACAGCTCTTATCTC 86612
QY 532 TGGCTATGTGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAAGTGT 591
Db 86611 TGGCTGTGTGCTGAATCTATGAGACATGATAGATTTGATGCAACAGAGGGGTAGTGT 86552
QY 592 TCTCTCCCTTACAGAAATGACATTTTAAATGCGATACAGTTAGATAGAAATATGACA 651
Db 86551 TCAGTGTCTTATGGAATGATATTTTACAGTGTATTTTAAAGGAGCGATTAAGTATGTA 86495
QY 652 TTAGAAAGGAGAAATGACAGGAGAAAGGAGAAAGGAGAAATTTGCCAAGGAAAAAAA 711
Db 86494 GGGAAAGGAAATATAAGGAGAAATGAGGAGAAATGAGGAGGAGACATGAACTGTAATA 86435
QY 712 AA 713
Db 86434 TA 86433

RESULT 9

AC112033
LOCUS
DEFINITION Rattus norvegicus clone CH230-94G2, *** SEQUENCING IN PROGRESS ***,
2 unordered pieces.
AC112033 273867 bp DNA linear HTG 10-OCT-2002

AC112033
 AC112033.3 GI:23667218
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
 Rattus norvegicus (Norway rat)
 SOURCE
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 273867)
 Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Dugan-Rochia,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
 Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
 Gunatane,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
 Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
 Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
 Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
 Kowals,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
 Lorusnewa,L., Loulsegue,H., Lozado,R.J., Lu,X., Ma,J.,
 Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
 Mahoney,S., McLeod,M.P., McNeill,T.Z., Meenan,E.,
 Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
 Morgan,M., Morris,K., Morris,S., Manidasa,M., Murphy,M., Nair,L.,
 Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
 Nwaokeme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
 Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
 Plopper,F., Polioz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,P.,
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
 Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
 Valas,R., Vera,V., Villalana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
 Williams,G., Williams,R., Wleczyk,R., Wooden,H., Worley,K.,
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstock,G. and Gibbs,R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 273867)
 Worley,K.C.
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 273867)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 10, 2002 this sequence version replaced gi:21737395.

***** Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GPBG
 Center clone name: CH230-94G2
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 244419 bases at least Q40
 Consensus quality: 247244 bases at least Q30
 Consensus quality: 249002 bases at least Q20
 Estimated insert size: 254595; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * As soon as it is available and the accession number will
 * be preserved.
 * 1 271836: contig of 271836 bp in length
 * 271837 271936: gap of unknown length
 * 271937 273867: contig of 1931 bp in length.
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 /db_xref="taxon:10116"
 /clone="CH230-94G2"
 1..1354
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 7780..8635
 /note="clone_boundary
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 site:EcoRI
 end_sequence:BH330629"
 7780..8511
 /note="clone_boundary
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 site:EcoRI
 end_sequence:BH330629"
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 clone_end:T7"
 site:EcoRI
 end_sequence:BH330629"
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 Best Local Similarity 71.7%; Pred. No. 1.2e-20;
 Matches 251; Conservative 0; Mismatches 89; Indels 10; Gaps 4;
 2 ATATATCATCTATTATTCATTAATCAATAATGTTATCT-TTTATTCATAACATTTGGG 60

45969 ATGTACCATTTATTTCTCATTAAAGATATAGGTGTCCTCCATGCTTCCATTAATATGG 46028
 61 TTTTGGGATTTTAAATTTTCAACACAGAGATGACATT-TTTTCTGTCATTATTTAT 119
 46029 TCTCTGCTTTTCAAGGATTTTCAAGGATTTTCAAGGATTTTCTTTTCTGTCATTGCTGT 46088
 120 TGTGCTGATGTGAAGCTATTTGGAGATCCATTCAGGAGCAACATTTGGAGATGGCT 179
 46089 TGTGACATATGAAGCATTTCCGAGATTTCAATTCAGGAGATATCCAGAGGAGAAAGACA 46148
 180 ACTTCTTATCAAGAAATTAAGAGACCAACAGTCAACCCACACAATCATCTTTAGAGACA 239
 46149 ACTTCCATCAAGAAATTAAGAGACCAACA---AACCCACAGCAATCTTTAGATGACA 46205
 240 GTGTGACTCTCAAGAGCTGTCAAAACACAGGCAAGGCAATAGTAAAGGA-----CG 294
 46206 AGGTGGCTCCCTCCAGGATCCCAACTACAGGCAAGGCAAGTAAAGGAGCAATGG 46265
 295 GAATCTTGACTCAAGAGGCTTAACTTTGCTGCTGAAGCTGGGCGAGG 344
 46266 GATCTCTGATCCAGAGGTTCAATTTCTGCTAGGCTGGGCTGGG 46315

RESULT 10
 AF400602
 LOCUS Homo sapiens beta-glucan receptor isoform H (BGR) mRNA, complete
 DEFINITION cds, alternatively spliced.
 ACCESSION AF400602
 VERSION AF400602.1 GI:15986713
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 881)
 AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
 TITLE Characterization of the human beta -glucan receptor and its
 alternatively spliced isoforms
 JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
 MEDLINE 21570237
 PUBMED 11567029
 REFERENCE 2 (bases 1 to 881)
 AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
 Oxford University, South Parks Road, Oxford OX1 3RE, UK
 FEATURES
 Location/Qualifiers
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 /map="12p13"
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 1..351
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 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 3.9e-19;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

132 AAGCTATTTGGAGATCCAAATTCAGGAAGCAACATTTGGAGATGGCTTCTTATCAA 191
 250 AAGCTATTTGGAGATCCAAATTCAGGAAGCAACATTTGGAGATGGCTTCTTATCAA 309
 192 GAAATAAGAGAACCAAGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCCTA 251
 310 GAAATAAGAGAACCAAGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCCTA 369
 252 CCAAGCTGTCAAAACACACAGG 273
 370 CCAAGCTGTCAAAACACACAGG 391

RESULT 11
 AF400597
 LOCUS Homo sapiens beta-glucan receptor isoform C (BGR) mRNA, complete
 DEFINITION cds, alternatively spliced.
 ACCESSION AF400597
 VERSION AF400597.1 GI:15986703
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 625)
 AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
 TITLE Characterization of the human beta -glucan receptor and its
 alternatively spliced isoforms
 JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
 MEDLINE 21570237
 PUBMED 11567029
 REFERENCE 2 (bases 1 to 625)
 AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
 TITLE Direct Submission
 JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
 Oxford University, South Parks Road, Oxford OX1 3RE, UK
 FEATURES
 Location/Qualifiers
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 1..570
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 SNELISDQNHSHYPRKPKISKLCMDSRVSHL"
 ORIGIN
 Query Match 19.6%; Score 140; DB 9; Length 625;
 Best Local Similarity 100.0%; Pred. No. 1e-18;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 2 (bases 1 to 744)
AUTHORS Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain
REFERENCE 3 (bases 1 to 744)
AUTHORS Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain
REMARK Sequence update by submitter
COMMENT On Oct 5, 2001 this sequence version replaced gi:14278818.
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DEFINITION cds, alternatively spliced.
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VERSION AF400601.1 GI:15986711
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 787)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
J. Biol. Chem. 276 (47), 43818-43823 (2001)
JOURNAL 21570237
MEDLINE 11567029
PUBMED
REFERENCE 2 (bases 1 to 787)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Direct Submission

JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology, Oxford University, South Parks Road, Oxford OX1 3RE, UK
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GenCore version 5.1.6
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874.330 Million cell updates/sec

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ALIGNMENTS

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; Sequence 376, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-06-25

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC62
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CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/088212

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RESULT 2

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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.

;; PRIOR FILING DATE: 1998-06-05
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3,38e-57 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-723-376 (1-713)

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Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHiser 40
Db 152 TCAGGAAGCAACACATTGGAGATGGCTACTTCTATCAAGAAATAAGAGAACACACAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 60
Db 212 CAACCCACACAATCATCTTTAGACAGAGTGTGACTCTCTACCAAGCTGCAAAACCA 271
Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GCGAAGGCGATAGTTAAAGACGGAATCTTGACTCAAGAGGGTTAATCTTGTGCTGAA 331

QY 81 AlaTtpGlyArgGlyValIlystysenThr 90
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RESULT 3

US-09-989-279-376
 ; Sequence 376, Application US/09989279
 ; Patent No. US2002007496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas P.
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C56
 ; CURRENT APPLICATION NUMBER: US/09/989,279
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00%
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US-09-989-293a-377 (1-90) x US-09-989-279-376 (1-713)
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Gaps: 0

; Sequence 376, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-07-09
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Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 61 GlyLysGlyLeuValLysGlyValArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 3,38e-57 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-731-376 (1-713)

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Db 92 ATGACATTTTCTCTGTCACCTATTATTATTGTTGGTATGTAAGCTATTTGGAGATCCAAT 151
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QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
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Db 152 TCAGGAGACACACATTTGGAGATGCTACTTCTATCAAGAAATAAAGAACACACAGT 211
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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
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Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAACACCA 271
|||
QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAapSerArgGlyLeuIleLeuGlyAlaGlu 80
|||
Db 272 GGCAGGGGCATAGTTAAAGACCGGAATCTTGACTCAAGAGGGTTAATCTTGTGTCTGAA 331
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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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Db 332 GCCTGGGCGAGGGGTGTAAAGAAAACACT 361
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RESULT 6

US-09-989-732-376
; Sequence 376, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-25

APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05

Alignment Scores:
Pred. No.: 3,38e-57 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-732-376 (1-713)

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QY 61 GlyLysGlyLysValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
DB 272 GCAAGGGGATATGTTAAAGGACGGAATCTTGACTCAAGAGGGTTAATCTTGTGTCTGAA 331
QY 81 AlaTyrGlyArgGlyValLysLysAsnThr 90
DB 332 GCTGGGGGCGGGGTGTAAAGAAAAAACAAT 361

RESULT 7

US-09-991-073-376
Sequence 376, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter

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/	PRIOR FILING DATE:	1998-07-01
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/	PRIOR APPLICATION NUMBER:	60/091978
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/	PRIOR APPLICATION NUMBER:	60/091982
/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/092182
/	PRIOR FILING DATE:	1998-07-09

Alignment Scores:	
Pred. No.:	3,38e-57
Score:	462.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Gaps:	0
Mismatches:	0
Conservative:	0
Matches:	713
Length:	713

US-09-989-293A-377 (1-90) x US-09-991-073-376 (1-713)

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Qy	21	SerGlySerAsnThrLeuGluAsnGlyYvrPheLeuSerArgAsnLysGluAsnHisser	40
Dd	152	TCAGGAGCAACACATTGGAGNATGGCTACTTTCTATCAAGAAATAAAGAGAACCACAGT	211
Qy	41	GlnProThrGlnSerSerIeuGluAspSerValThrProThrLysAlaValLysThrThr	60
Dd	212	CRACCACACAATCATCTTTTAGAACACAGTGTAAGCTCTCTACCAAAGCTGTCAAAACACCA	271
Qy	61	GlyIysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeulleLeuGlyAlaGlu	80
Dd	272	GGCAAGGGCATAGTTAAAGAGCGGAATCTTGACTCAAGAGGGTTAAITCTTTGGTGCTGAA	331
Qy	81	AlatrpGlyIargGlyVallyLysLysAsnthr	90
Dd	332	GCCTTGGGSCAGGGCTGTAAAGAAAACACT	361

RESULT 8
US-09-990-442-376
Sequence 376, Application US/09990442
Patent No. US20020132252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavins, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3.28e-57
Score: 462.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

US-09-989-293A-377 (1-90) x US-09-990-442-376 (1-713)

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; PRIOR FILING DATE: 1998-07-09

US-09-991-163-376
; Sequence 376, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Stewart, Timothy A.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3,38e-57 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-993-604-376 (1-713)

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QY 81 AlaTrpGlyArgGlyValIysLysAsnThr 90
Db 332 GCGTGGGGCAGGGGTGTAAGAAAAACACT 361

RESULT 11
US-09-990-456-376
; Sequence 376, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin I.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zeman
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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Query Match: 100.00% Indels: 0
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Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Godowski, Paul J.

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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 3,38e-57 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-992-598-376 (1-713)

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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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RESULT 14
US-09-989-293A-376
; Sequence 376, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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Alignment Scores:		
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Score:	462.00	Matches: 90
Percent Similarity:	100.00%	Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
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US-09-989-293A-377 (1-90) x US-09-989-293A-376 (1-713)

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DB 92 ATGACATTTTCTGTCACATATATATTGTTGGTATGTGAAGCTATTTGGAGAACCAT 151
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DB 152 TCAGGAAGCACACACATTGGAGATGGCTACTTTCTATCAAGAAATTAAGAGAACCACT 211
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
DB 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCCACCAAGAGCTGTCAAAACCA 271
QY 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
DB 272 GGCAGGGCATAGCTTAAGAGACGGAATCTTGACTCAAGAGGGTTAATCTTGGTGTGAA 331
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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RESULT 15

US-09-989-735-376
Sequence 376, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
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CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

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US-09-989-293A-377 (1-90) x US-09-989-735-376 (1-713)

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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACA 271
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Db 272 GCAAGGGGCATAGTTAAGGACGGAACTCTTGACTCAAGAGGGTTAATTTCTTGTGCTGAA 331
QY 81 AlaTyrGlyArgGlyValLysLysAsnThr 90
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Search completed: April 4, 2004, 10:58:42
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: April 4, 2004, 07:58:52 ; Search time 89 Seconds
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561.186 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

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Fgapop 6.0 , Fgapext 7.0
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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3	70.5	15.3	1799	US-08-560-398-3	Sequence 3, Appli
4	69.5	15.0	2271	US-09-205-258-243	Sequence 243, App
5	69.5	15.0	2276	US-09-205-258-183	Sequence 183, App
6	67.5	14.6	849	US-09-107-532A-1899	Sequence 1899, Ap
7	67	14.5	804	US-09-242-690A-35	Sequence 35, Appl
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10	67	14.5	2330	US-09-242-690A-34	Sequence 34, Appl
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12	66.5	14.4	1065	US-09-252-991A-16320	Sequence 16320, A

C 13	66.5	14.4	1332	4	US-09-252-991A-15961	Sequence 15961, A
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C 15	65.5	14.2	744	4	US-09-134-000C-2940	Sequence 2940, Ap
C 16	65.5	14.2	1341	4	US-09-252-991A-16544	Sequence 16544, A
C 17	65	14.1	1386	4	US-09-134-001C-767	Sequence 767, App
C 18	65	14.1	2003	4	US-09-148-545-109	Sequence 109, App
C 19	65	14.1	2070	4	US-09-148-545-51	Sequence 51, Appl
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C 28	64	13.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
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C 41	62	13.4	3054	4	US-09-762-724-11	Sequence 11, Appli
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ALIGNMENTS

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; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; FILING DATE: US/08/772,440
; APPLICATION NUMBER: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2298 base pairs
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US-08-772-440-1

Alignment Scores:
Pred. No.: 9,48e-10 Length: 2298
Score: 143.50 Matches: 29
Percent Similarity: 74.47% Conservatives: 6
Best Local Similarity: 61.70% Mismatches: 11
Query Match: 31.06% Indels: 1
DB: Gaps: 1

US-09-989-293A-377 (1-90) x US-08-772-440-1 (1-2298)
QY 15 AlaileTtpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34
Db 290 GCATTTGGCGACACAAATTCAGGAGAAATCCAGAGGAGAAAGACAACTTCCTATCAAGA 349
QY 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54
Db 350 AATAAGAGAACACAC---AAGCCCAAGAAATCATCTTTAGATGAGAGAGGTGGCTCCCTCC 406
QY 55 LysAlaValLysThrThrGly 61
Db 407 AAGGCATCCCAACTACAGGA 427

RESULT 2
US-08-772-440-7
; Sequence 7, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: CDS
; LOCATION: 291..1571
; OTHER INFORMATION: /note= "clone O40 ovule-specific gene
; OTHER INFORMATION: encoding a cytochrome P450 monooxygenase
; OTHER INFORMATION: from pollen tubes of Phalaenopsis"
US-08-560-398-3
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US-08-772-440-7

Alignment Scores:
Pred. No.: 3,64e-10 Length: 528
Score: 139.50 Matches: 28
Percent Similarity: 75.56% Conservatives: 6
Best Local Similarity: 62.22% Mismatches: 10
Query Match: 30.19% Indels: 1
DB: Gaps: 1

US-09-989-293A-377 (1-90) x US-08-772-440-7 (1-528)
QY 17 TtpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLys 36
Db 4 TGGCGACACAAATTCAGGAGAAATCCAGAGGAGAAAGACAACTTCCTATCAAGAAATAAA 63
QY 37 GluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysala 56
Db 64 GAGAAACAC---AAGCCCAAGAAATCATCTTTAGATGAGAGAGGTGGCTCCCTCCAAAGCA 120
QY 57 ValLysThrThrGly 61
Db 121 TCCCAAACTACAGGA 135

RESULT 3
US-08-560-398-3/c
; Sequence 3, Application US/08560398
; Patent No. 5907082
; GENERAL INFORMATION:
; APPLICANT: O'Neill, Sharman
; APPLICANT: Nadeau, Jeanette
; TITLE OF INVENTION: Ovule-Specific Gene Expression
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,398
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-063300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 19..23
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1571
; OTHER INFORMATION: /note= "clone O40 ovule-specific gene
; OTHER INFORMATION: encoding a cytochrome P450 monooxygenase
; OTHER INFORMATION: from pollen tubes of Phalaenopsis"
US-08-560-398-3
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/ EARLIER APPLICATION NUMBER: 60/048,900
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,901
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,892
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,915
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,019
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,970
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,972
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,916
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,373
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,875
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,374
/ EARLIER FILING DATE: 1997-05-06
/ EARLIER APPLICATION NUMBER: 60/048,917
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,949
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,893
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,897
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,898
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,962
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 243
/
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (553)
/ OTHER INFORMATION: n equals a,t,g, or c
/
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (2267)
/ OTHER INFORMATION: n equals a,t,g, or c
/
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (2269)
/ OTHER INFORMATION: n equals a,t,g, or c
/
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (2271)
/ OTHER INFORMATION: n equals a,t,g, or c
/
/ US-09-205-258-243
/
/ Alignment Scores:

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Pred. No.: 17 Length: 2271
Score: 69.50 Matches: 21
Percent Similarity: 53.03% Conservative: 14
Best Local Similarity: 31.82% Mismatches: 22
Query Match: 15.04% Indels: 9
DB: 4 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-205-258-243 (1-2271)

QY 5 LeuSerLeuLeuLeuLeuValcysGluAla-----lleTrpArgSerAsn 20
Db 151 CTGGTCTTGGCGCTCCTGCTGTGTGTCGCCGCTCTATCCAGTGTGTATCACGGACTGAT 210
QY 21 SerGlySerAsnThrLeuGluAsnclYrPheLeuSerArgAsn----- 35
Db 211 TCACCGAGCCCAACCGTACTCACTCAATATTTCTACCCCAATGTGAATGCTTTAAACA 270
QY 36 LysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLys 55
Db 271 CATGAAACCAAAACCAAACTTCTATTTCCCAATTCAGACACACCTCCCTCCACGACG 330
QY 56 AlaValLysThrThrGly 61
Db 331 AGTACCAGAAAAGTGA 348

RESULT 5
US-09-205-258-183
; Sequence 183, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06

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/	EARLIER APPLICATION NUMBER:	60/048,915
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/049,019
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,970
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,972
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,916
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/049,373
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,875
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/049,374
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,917
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,949
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,974
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,883
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,897
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,898
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,962
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,963
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,877
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/048,878
/	EARLIER FILING DATE:	1997-06-06
/	EARLIER APPLICATION NUMBER:	60/070,923
/	EARLIER FILING DATE:	1997-12-18
/	EARLIER APPLICATION NUMBER:	60/092,921
/	EARLIER FILING DATE:	1998-07-15
/	EARLIER APPLICATION NUMBER:	60/094,657
/	EARLIER FILING DATE:	1998-07-30
/	NUMBER OF SEQ ID NOS:	1227
/	SOFTWARE:	PatentIn Ver. 2.0
/	SEQ ID NO 183	
/	LENGTH:	2276
/	TYPE:	DNA
/	ORGANISM:	Homo sapiens
/	US-09-205-258-183	
Alignment Scores:		
Pred. No.:	17	Length: 2276
Score:	69.50	Matches: 21
Percent Similarity:	53.03%	Conservative: 14
Best Local Similarity:	31.82%	Mismatches: 22
Query Match:	15.04%	Indels: 9
DB:	4	Gaps: 2
US-09-989-293A-377 (1-90) x US-09-205-258-183 (1-2276)		
Qy	5 LeuSerLeuLeuLeuLeuValCysGluAla-----IleTrpArgSerAsn 20	::: :::
Db	160 CTGGTCTGGCGCTCCGTCTGTTCGCCGCCTATCCAGTGTTGTATCACGGACTGAT 219	::: :::
Qy	21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsn----- 35	::: :::
Db	220 TCACCGAGCCCAACCGTACTCAACTCATATTCTACCCCAAATGTGAATGCTTTAAACA 279	::: :::
Qy	36 LysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLys 55	::: :::
Db	280 CATGAATAACCAAAACAAACCTTCTATTTCCCAANTCAGACACCACCTCCCTCCCACGACG 339	::: :::
Ov	56 AlaVallYsThrThrGly 61	

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Db 340 AGTACCAAGAAAAGTGG 357
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RESULT 6
US-09-107-532A-1899/c
; Sequence 1899, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...849
; SEQUENCE DESCRIPTION: SEQ ID NO: 1899:
US-09-107-532A-1899
Alignment Scores:
Pred. No.: 7.21 Length: 849
Score: 67.50 Matches: 24
Percent Similarity: 41.84% Conservative: 17
Best Local Similarity: 24.49% Mismatches: 29
Query Match: 14.61% Indels: 28
DB: 4 Gaps: 2
US-09-989-293A-377 (1-90) x US-09-107-532A-1899 (1-849)
Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn-ThrLeuGlu 27
::: ||| ::||
Db 527 ATCTTGATCTGCTGTTCTGAAATTTTGTGAGCAATCGAGGCATAATGCAATGCG 468
::: ||| ::||
Qy 27 uAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGlnSerSer-- 46
::: ||| ::||
Db 467 GAGACAGTATCCAGATTCATCAAGAGAAGCTTAAACCAACCAACCCAGCCTTCCAC 408
::: ||| ::||
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Qy 47 -----LeuGluAspSerValThrProThry 55
::: ||| ::||
Db 407 TGAAGGGCTCAATCGAAATTTGAGAAAGATAGATTGAAGAGCGCCAGCTGCCAACCA 348
::: ||| ::||
Qy 55 s-----AlaVallysthTh 60
::: ||| ::||
Db 347 ACAGCAAAACCTGCTGTCATAAAGGAATAACGGATGAAATCTTGAATAATTTGTTAAT 288
::: ||| ::||
Qy 60 rGlyLysGlyIleVallysglyArgAsnLeuAspSerArgGlyLeuLeu 77
::: ||| ::||
Db 287 TGGTGAAAAGGCTTACATGCGGAGAACTTAATCTACTGAACGTTTTTTA 236
::: ||| ::||
RESULT 7
US-09-242-690A-35
; Sequence 35, Application US/09242690A
; Patent No. 6284534
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/242,690A
; CURRENT FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02924
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 35
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Candida utilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(801)
US-09-242-690A-35
Alignment Scores:
Pred. No.: 7.78 Length: 804
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 3 Gaps: 2
US-09-989-293A-377 (1-90) x US-09-242-690A-35 (1-804)
Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
::: ||| ::||
Db 218 CTACTGTGGCTCCACTGTTGGAGCTTTCAAAGAACACAAATTCCTCATCTTTGAGAGACC 277
::: ||| ::||
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
::: ||| ::||
Db 278 GTAAGTTTCTGATATCGGCAACACCGTCACGCGGTGGTGGCTTCAAGA 337
::: ||| ::||
Qy 47 LeuGluAspSerValThrProThrysAlaVallysthThrGlyLysGlyIleVally 66
::: ||| ::||
Db 338 TTGCGCAATGGGCGAGATATC-ACCAACGCCGCCAGGTGTCCACCGTCAGATCGCAAG 396
::: ||| ::||
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
::: ||| ::||
Db 397 GGGTTGAAGAGAGCTCCACAGGAACACCGATGAGCGGCTGTTGATGCTTGGC 456
::: ||| ::||
Qy 80 GluAlaTrpGlyArgGly 85
::: ||| ::||
Db 457 GAGCTGAGCTCCCAAGGCGC 474
::: ||| ::||
RESULT 8
US-09-908-855-35
; Sequence 35, Application US/09908855
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; Patent No. 6610514
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; FILE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/908,855
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/242,690
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Candida utilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(801)
US-09-908-855-35

Alignment Scores:
Pred. No.: 7.78 Length: 804
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 4 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-908-855-35 (1-804)

Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 218 CTACTGGCTCCACTGTGGAGCTTCAAGAGACAAATTTCTCATCTTTGAGACC 277
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSer 46
Db 278 GTAAGTTTGCTGATATCGGCACACCGTCACAGGCACAGTACGCCGGTGGTTCAGA 337
Qy 47 LeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGlyLeValLys 66
Db 338 TTGCGCAATGGCGAGATATC-ACCAACGCCCAACCGTGTCCACCGTGCAGGTATCGTCAAG 396
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 397 GGGTTGAGAGGCTGCACAGGAACCCAGGATGACGACAGAGGGCTGTGATGCTTGGC 456
Qy 80 GluAlaTrpGlyArgGly 85
Db 457 GAGCTGAGCTCCAAGGC 474

RESULT 9
US-08-557-128-3
; Sequence 3, Application US/08557128
; Patent No. 5849524
; GENERAL INFORMATION:
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: MISA, No. 5849524ihiko
; TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
; TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
; TITLE OF INVENTION: THEREWITH
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Hardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,128
; FILING DATE: 25-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP95/01005
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-129287
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-285823
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-135015
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1259..2059
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1259..2059
; US-08-557-128-3

Alignment Scores:
Pred. No.: 39.2 Length: 2330
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 2 Gaps: 2

US-09-989-293A-377 (1-90) x US-08-557-128-3 (1-2330)

Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 1476 CTACTGGCTCCACTGTGGAGCTTCAAGAGACAAATTTCTCATCTTTGAGACC 1535
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSer 46
Db 1536 GTAAGTTTGCTGATATCGGCACACCGTCACAGGCACAGTACGCCGGTGGTTCAGA 1595
Qy 47 LeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGlyLeValLys 66
Db 1596 TTGCGCAATGGCGAGATATC-ACCAACGCCCAACCGTGTCCACCGTGCAGGTATCGTCAAG 1654
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 1655 GGGTTGAGAGGCTGCACAGGAACCCAGGATGACGACAGAGGGCTGTGATGCTTGGC 1714
Qy 80 GluAlaTrpGlyArgGly 85
Db 1715 GAGCTGAGCTCCAAGGC 1732
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Db 268 TCGGCGAAGGCTCCGACCGACCCCTGGCGAGCGCGAGAGTTTCATCGCTCGGACC 327
Qy 55 -----LysAlaValLysThrGlyLysGlyIleVal 65
Db 328 CGCGCGACAGCGGFTGCCCTGGGCGATGACGACGCGGGTCTGCTCAGTGCCTGGTG 387
Qy 66 LysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAla 79
Db 388 CGCGGGGCAACTCGACTTCGAAGGCATCGCTCGCATGCC 429

RESULT 13

US-09-252-991A-15961/c
; Sequence 15961, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15961
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15961

Alignment Scores:

Pred. No.: 19.7 Length: 1332
Score: 66.50 Matches: 19
Percent Similarity: 41.89% Conservative: 12
Best Local Similarity: 25.68% Mismatches: 32
Query Match: 14.39% Indels: 11
DB: 4 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-252-991A-15961 (1-1332)

Qy 15 AlaIleTrpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34
Db 885 GCCTGTGTGACGGTTTCCGACCGCGACGAT-----GACCGCTGTATCGCTCGCAACC 832
Qy 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54
Db 831 TCGGCGAAGGCTCCGACACCGCCCTGGCAGCGCGAGCGGATTCATCGCTCGGACC 772
Qy 55 -----LysAlaValLysThrGlyLysGlyIleVal 65
Db 771 CGCGCGACAGCGGTTGCCCTGGGCGATGACGACGCGGCTCTGGCTCAGTGCCTGGTG 712
Qy 66 LysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAla 79
Db 711 CGCGGGGCAACTCGACTTCGAAGGCATCGCTCGCATGCC 670

RESULT 14

US-09-621-976-3007/c
; Sequence 3007, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pdm
; SEQ ID NO 3007

; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..453
US-09-621-976-3007
Alignment Scores:
Pred. No.: 7.02 Length: 548
Score: 65.50 Matches: 17
Percent Similarity: 54.39% Conservative: 14
Best Local Similarity: 29.82% Mismatches: 23
Query Match: 14.18% Indels: 3
DB: 4 Gaps: 1
US-09-989-293A-377 (1-90) x US-09-621-976-3007 (1-548)
Qy 4 PheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySer 23
Db 504 TACCTCACCTCACATTGCTATTACGATTCAAAGCCTCCATAAACTGTCAAACCTGGCAG 445
Qy 24 AsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThr 43
Db 444 AACACAGAGAAACCATGGGCATTTCTTCCACAGGGTTTGAACACCATCAACGCTCTAGT 385
Qy 44 GlnSerSerLeuGlu-----AspSerValThrProThrLysAlaVal 57
Db 384 CCTGTTGACCTGGAAATGGTGGCAGGTGAAGTCTCTCCACACGATGCCTTG 334

RESULT 15

US-09-134-000C-2940
; Sequence 2940, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2940
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2940

Alignment Scores:
Pred. No.: 11.2 Length: 744
Score: 65.50 Matches: 16
Percent Similarity: 44.23% Conservative: 7
Best Local Similarity: 30.77% Mismatches: 14
Query Match: 14.18% Indels: 15
DB: 4 Gaps: 1
US-09-989-293A-377 (1-90) x US-09-134-000C-2940 (1-744)

Qy 27 GluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGlnSerSer 46
Db 553 GAAAAGAGTACCTGATTAAAGAAAGGTACCGATTGGAATGCTACACAGAGTCA 612
Qy 47 Leu-----GluAspSerVal 51
Db 613 ATGGATCTCGAATTATTGAAGTGAAGAAAGACGATTTGCGACGTTCCGATGGTAGTGA 672
Qy 52 ThrProThrLysAlaValLysThrGlyLysGly 63
Db 673 AGTATCATGTAACGCGCTTAAGTTACTCTGGGAAAGGT 708

Search completed: April 4, 2004, 09:55:54
Job time : 97 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2004, 06:59:37 ; Search time 428 Seconds
(without alignments)
893.313 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

Sequence: 1 MTFPFLSLILLVCEAIWRSN.....DSRGLILGAEAWGRGVKKNT 90

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: Geneseqn2000s: *
4: Geneseqn2001as: *
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6: Geneseqn2002s: *
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8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	712	5 AAC91481	Aac91481 Human PRO
2	462	100.0	713	3 AAZ65094	Aaz65094 Membrane-
3	462	100.0	713	3 AAC58634	Aac58634 Human PRO
4	462	100.0	713	4 AAS21480	Aas21480 Human CDN
5	462	100.0	713	5 AAF44240	Aaf44240 Human PRO
6	462	100.0	713	7 ABX77952	Abx77952 Human PRO
7	462	100.0	713	7 ABX80364	Abx80364 Novel hum
8	462	100.0	713	7 ACA69270	ACA69270 Human CDN

9	462	100.0	713	7 ACD24089	AcD24089 Novel hum
10	462	100.0	713	7 ABX90341	Abx90341 Human sec
11	462	100.0	713	7 ABX64187	Abx64187 cDNA enco
12	462	100.0	713	7 ACA67230	ACA67230 cDNA enco
13	462	100.0	713	7 ACA64409	ACA64409 Novel hum
14	462	100.0	713	7 ACA03839	ACA03839 cDNA enco
15	462	100.0	713	7 ABX89377	Abx89377 DNA enco
16	462	100.0	713	7 ABX80868	Abx80868 Human sec
17	462	100.0	713	7 ACD44377	ACD44377 cDNA enco
18	462	100.0	713	7 ACD42031	ACD42031 Human sec
19	462	100.0	713	7 ABX79548	Abx79548 Human sec
20	462	100.0	713	7 ACA93569	ACA93569 Novel hum
21	462	100.0	713	7 ABX81251	Abx81251 Novel hum
22	462	100.0	713	7 ACA04260	ACA04260 Human CDN
23	462	100.0	713	7 ACA93067	ACA93067 Novel hum
24	462	100.0	713	7 ABX17151	Abx17151 Human PRO
25	462	100.0	713	8 ACA68006	ACA68006 Novel hum
26	462	100.0	713	8 ACA88455	ACA88455 Human sec
27	462	100.0	713	8 ACD81962	ACD81962 cDNA enco
28	462	100.0	713	8 ADA45992	ADA45992 Novel hum
29	462	100.0	713	8 ADA76423	ADA76423 Human PRO
30	462	100.0	713	8 ADA19073	ADA19073 Human PRO
31	462	100.0	713	8 ADA61696	ADA61696 Homo sapi
32	462	100.0	713	8 ADB19481	ADB19481 Novel hum
33	462	100.0	713	8 ADB28022	ADB28022 cDNA enco
34	462	100.0	713	8 ADA86501	ADA86501 Novel hum
35	462	100.0	713	8 ADB16065	ADB16065 Human PRO
36	462	100.0	713	8 ADA37887	ADA37887 Human CDN
37	462	100.0	713	8 ADA47851	ADA47851 Human PRO
38	462	100.0	713	8 ADA21573	ADA21573 Human CDN
39	462	100.0	713	8 ADA10360	ADA10360 Human CDN
40	462	100.0	713	8 ADA67646	ADA67646 Human PRO
41	462	100.0	713	8 ADR30653	ADR30653 cDNA enco
42	462	100.0	713	8 ADA85349	ADA85349 Novel hum
43	462	100.0	713	8 ADA17904	ADA17904 cDNA enco
44	462	100.0	713	8 ADA97161	ADA97161 Human PRO
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ALIGNMENTS

RESULT 1
AAC91481
ID AAC91481 standard; cDNA; 712 BP.

XX AC AAC91481;

XX AC AAC91481;

DT 21-MAR-2001 (first entry)

XX Human PRO1159 cDNA.

DE Human; PRO; antiinflammatory; dermatological; antiarthritic;

KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;

KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;

KW antiallergic; antiasthmatic; immune related disorder;

KW hepatobiliary disease; autoimmune disease; allergy; ss.

XX Homo sapiens.

XX WO200073452-A2.

XX 07-DEC-2000.

XX 02-JUN-2000; 2000WO-US015264.

XX 02-JUN-1999; 99WO-US012252.

XX 20-JUL-1999; 99US-0144732P.

XX 20-JUL-1999; 99US-0144758P.

XX 28-JUL-1999; 99US-0146222P.

XX 01-SEP-1999; 99WO-US020111.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 29-OCT-1999; 99US-0162506P.

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PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 20-DEC-1999; 99WO-US030913.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
XX PA
XX (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;
XX PI Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;
XX PI Watanabe CK, Wood WI,
XX
XX WPI; 2001-025253/03.
XX P-PSDB; AAB50922.
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful in
XX PT the diagnosis and treatment of immune related disorders, e.g. systemic
XX PT lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis
XX PT and diabetes mellitus.
XX
XX Claim 48; Fig 41; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
XX CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
XX CC antagonists are useful for treating and diagnosing immune related
XX CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX CC immune-mediated renal disease, demyelinating diseases of the central and
XX CC peripheral nervous systems (such as multiple sclerosis, idiopathic
XX CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
XX CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such
XX CC as infectious, autoimmune chronic active hepatitis, primary biliary
XX CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX CC disease, autoimmune or immune-mediated skin diseases (such as bullous
XX CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX CC food hypersensitivity and urticaria), immunological diseases of the lung
XX CC (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
XX CC hypersensitivity pneumonitis), transplantation associated diseases
XX CC including graft rejection and graft-versus-host diseases
XX
XX SQ Sequence 712 BP; 262 A; 105 C; 134 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,03e-52 Length: 712
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

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 QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
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 Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACACACAGT 211
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 QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
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 Db 212 CAACCCACACAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACA 271
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 QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
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 Db 272 GGCAAGGGCAGTAGTTTAAAGGACGGGAATCTTGACTCAGAGGGTTAAATCTTGGTCTGCTGAA 331
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 QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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 Db 332 GCTGGGGCAGGGGGTGTAAGAGAAACACACT 361
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RESULT 2
 AAZ65094
 ID AAZ65094 standard; cDNA; 713 BP.
 XX
 AC AAZ65094;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1159 encoding cDNA.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9963088-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US012252.
 XX
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
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 PR 04-JUN-1998; 98US-0088328P.
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 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
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 PR 11-JUN-1998; 98US-0088858P.
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PR 11-JUN-1998; 98US-0088863P.
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PR 12-JUN-1998; 98US-0089090P.
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PR 18-JUN-1998; 98US-0089801P.
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PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
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PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
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PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
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PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
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PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
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PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095923P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 31-AUG-1998; 98US-0098014P.
PR 16-SEP-1998; 98US-0098525P.
PR 12-JAN-1999; 99US-0115565P.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX WFI; 2000-072883/06.
XX P-PSDB; AAY66748.
XX
XX Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 271; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
XX
XX SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-989-293A-377 (1-90) x AAZ65094 (1-713)
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```
QY 1 MetThrPheLeuSerLeuLeuLeuLeuValCysGluAlaIleTTPArgSerAsn 20
Db 92 ATGACATTTTCTGCTACTATTATTATTTGGTATGTGAAGCTATTGTGAGATCCCAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCACACATTGGAGATGGCTACTTCTCTATCAAGAAATAAGAGACACACAGT 211
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGACAGACAGTGTGACTCTACCAAGCTGTCAAAACCCACA 271
QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyAlaGlu 80
Db 272 GCGAAGGGCATAGTTAAAGACGCGAATCTTGACTCAAGAGGGTTAATTTCTTGGTCTGAA 331
QY 81 AlaTTPGlyArgGlyValLysLysAsnThr 90
Db 332 GCGTGGGCGAGGGGTGAAGAAACACT 361
RESULT 3
AAC58634
ID AAC58634 standard; cDNA; 713 BP.
XX
AC AAC58634;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.
XX
KW Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW Graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
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PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI: 2000-572271/53.
DR P-PSDB; AAB33469.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 23; Fig 111; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-989-293A-377 (1-90) x AAC58634 (1-713)
QY 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTTPArgSerAsn 20
Db 92 ATGACATTTTCTGCTACTATTATTATTTGGTATGTGAAGCTATTGTGAGATCCCAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
```

Db 152 TCAGGAGCAACATCTGGAGATGGCTACTTCTATCAAGAAATAAGAGAACACAGT 211
 Qy 41 GlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
 Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACCA 271
 Qy 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyValaGlu 80
 Db 272 GGCAGGGGCTAGTAAAGGACGGAATCTTCTGACTCAAGAGGGTTAAATCTTTGGTGTGAA 331
 Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
 Db 332 GCCTGGGCGAGGGGTGTAAAGAAAACACT 361
 RESULT 4
 ID AAS21480 standard; cDNA; 713 BP.
 XX
 AC AAS21480;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human cDNA sequence encoding for PRO1159 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US032678.
 XX
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005061.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2001-408281/43.
 DR P-PSDB; AAU12408.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3; Fig 473; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,04e-52 Length: 713
 Score: 462.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-989-293A-377 (1-90) x AAS21480 (1-713)
 Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
 Db 92 ATGACATTTTTTCTGTCTATTTATTTATTTGGTATGGAAGCTATTTGGAGATCCAT 151
 Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
 Db 152 TCAGGAGCAACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACCA 211
 Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
 Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACCA 271
 Qy 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyValaGlu 80
 Db 272 GGCAGGGGCTAGTAAAGGACGGAATCTTCTGACTCAAGAGGGTTAAATCTTTGGTGTGAA 331
 Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
 Db 332 GCCTGGGCGAGGGGTGTAAAGAAAACACT 361

CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44270 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
 CC AAF65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores: Length: 713
 Pred. No.: 6.04e-52 Matches: 90
 Score: 462.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 5

US-09-989-293A-377 (1-90) x AAF44240 (1-713)

QY 1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
 Db 92 ATGACATTTTCTGTCACCTATTATTGTTGTTGATGCTGAAGCTATTGAGATCCAAT 151

QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
 Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAGAAATAAAGAGAACACAGT 211

QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
 Db 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCA 271

QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
 Db 272 GGCAGGGGCATAGTTAAAGGACCGAATCTTGACTCAGAGGGTTAAATCTTGGTGTGAA 331

QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
 Db 332 GCCTGGGGCAGGGGTGTAAGAAAAACACT 361

RESULT 6
 ABX77952
 ID ABX77952 standard; cDNA; 713 BP.
 AC ABX77952;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human PRO polynucleotide #118.
 XX
 KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
 KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003027163-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 15-NOV-2001; 2001US-00997666.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020069.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.

RESULT 5
 AAF44240
 ID AAF44240 standard; cDNA; 713 BP.
 XX
 AC AAF44240;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW cancer; chromosomal mapping; Gene mapping; tissue typing;
 KW diagnostic assay; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0153663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US005884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart IA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 WPI; 2001-032160/04.
 DR P-PSDB; AAB65271.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX
 PS Claim 2; Fig 271; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating

PR	02-JUN-1998;	98US-0087759P.	PR	07-JUL-1998;	98US-0091982P.
PR	03-JUN-1998;	98US-0087827P.	PR	09-JUL-1998;	98US-0092182P.
PR	04-JUN-1998;	98US-0088021P.	PR	10-JUL-1998;	98US-0092472P.
PR	04-JUN-1998;	98US-0088025P.	PR	20-JUL-1998;	98US-0093333P.
PR	04-JUN-1998;	98US-0088026P.	PR	30-JUL-1998;	98US-0094651P.
PR	04-JUN-1998;	98US-0088028P.	PR	04-AUG-1998;	98US-0095282P.
PR	04-JUN-1998;	98US-0088029P.	PR	04-AUG-1998;	98US-0095285P.
PR	04-JUN-1998;	98US-0088030P.	PR	04-AUG-1998;	98US-0095301P.
PR	04-JUN-1998;	98US-0088033P.	PR	04-AUG-1998;	98US-0095302P.
PR	04-JUN-1998;	98US-0088326P.	PR	04-AUG-1998;	98US-0095318P.
PR	05-JUN-1998;	98US-0088167P.	PR	04-AUG-1998;	98US-0095321P.
PR	05-JUN-1998;	98US-0088202P.	PR	04-AUG-1998;	98US-0095325P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-AUG-1998;	98US-0095916P.
PR	05-JUN-1998;	98US-0088217P.	PR	10-AUG-1998;	98US-0095929P.
PR	09-JUN-1998;	98US-0088655P.	PR	10-AUG-1998;	98US-0096012P.
PR	10-JUN-1998;	98US-0088734P.	PR	11-AUG-1998;	98US-0096143P.
PR	10-JUN-1998;	98US-0088738P.	PR	11-AUG-1998;	98US-0096146P.
PR	10-JUN-1998;	98US-0088742P.	PR	12-AUG-1998;	98US-0096329P.
PR	10-JUN-1998;	98US-0088810P.	PR	17-AUG-1998;	98US-0096757P.
PR	10-JUN-1998;	98US-0088824P.	PR	17-AUG-1998;	98US-0096766P.
PR	10-JUN-1998;	98US-0088826P.	PR	17-AUG-1998;	98US-0096771P.
PR	11-JUN-1998;	98US-0088858P.	PR	17-AUG-1998;	98US-0096773P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-AUG-1998;	98US-0096791P.
PR	11-JUN-1998;	98US-0088876P.	PR	17-AUG-1998;	98US-0096867P.
PR	12-JUN-1998;	98US-0089105P.	PR	17-AUG-1998;	98US-0096891P.
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XX	PR	16-JUN-1997; 97US-0049787P;
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PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
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PR 03-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX Abkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PU;
PI Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WI;
PI Zhang Z;
XX
XX WPI; 2003-247083/24.
DR P-PSDB; ABUS9165.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
XX Claim 2; Fig 273; 648pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO543, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the

CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluHisSer 40
DB 152 TCAGGAGACACACATCTGGAGATGCTACTTCTTATCAAGAAATAAGAGAACACACAGT 211
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
DB 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACACA 271
QY 61 GlyLysGlyLysValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyAlaGlu 80
DB 272 GGCAGGGGCATATTAAAGACGGATCTTGATCTCAGAGGGTTAATCTTGTGTCTGAA 331
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
DB 332 GCCTGGGGCAGGGGTGTAAAGAAACACT 361
RESULT 8
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ID ACA69270 standard; cDNA; 713 BP.
XX
XX ACA69270;
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XX 26-JUN-2003 (first entry)
XX Human cDNA encoding secreted/transmembrane protein PRO1159.
XX
XX Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosa; age-related macular degeneration; AMD;
KW kidney disease; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX
XX Homo sapiens.
XX US2003032023-A1.
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XX 13-FEB-2003.
XX
XX 14-NOV-2001; 2001US-00990711.
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XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
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PR 12-NOV-1997; 97US-0065186P.
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PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
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PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
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PR 11-AUG-2000; 2000WO-US020231.
PR 11-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

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Percent Similarity: 100.00%
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RESULT 9
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XX
DT 26-AUG-2003 (first entry)
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XX Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antihypertensive; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing; gene; ss.
XX
OS Homo sapiens.
XX

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PN US2003032156-A1.
XX 13-FEB-2003.
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PR 12-JUN-1998; 98WO-US012456.
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PR 29-OCT-1998; 98WO-US022992.
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PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
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PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
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PR 20-DEC-1999; 99WO-US030999.
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PR 05-JAN-2000; 2000WO-US000219.
PR 05-JAN-2000; 2000WO-US000377.
PR 06-JAN-2000; 2000WO-US000376.
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PR 22-FEB-2000; 2000WO-US004414.
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PR 23-AUG-2000; 2000WO-US023322.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00809689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
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PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341980/32.
XX P-PSDB; AB017852.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
XX inflammation, organ failure, atherosclerosis, cardiac injury,
XX infertility, birth defects, premature aging, acquired immunodeficiency
XX syndrome (AIDS), or cancer.
XX
XX Claim 2; Fig 473; 660pp; English.
XX
XX The invention describes an isolated nucleic acid (I) comprising, or which
XX has 80 % sequence identity to, or the full-length coding sequence of, one
XX of 275 nucleotide sequences, and which encodes a corresponding
XX polypeptide selected from 275 amino acid sequences, where all sequences
XX are given in the specification. The polypeptide encoded by (I) is used to
XX detect PRO polypeptides, link a bioactive molecule to a cell expressing a
XX PRO polypeptide, modulate a biological activity of a cell, stimulate the
XX release of tumour necrosis factor (TNF)-alpha from human blood, modulate
XX the uptake of glucose or free fatty acid by cells, stimulate or inhibit
XX the proliferation or differentiation of cells or gene expression,
XX stimulate the release of proteoglycans, stimulate the release of cytokine
XX from peripheral blood mononuclear cells, inhibit the binding of A-peptide
XX to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
XX acid and polypeptide encoded by it are useful for treating inflammatory
XX diseases, organ failure, atherosclerosis, cardiac injury, infertility,
XX birth defects, premature aging, acquired immunodeficiency syndrome
XX (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
XX hybridisation probes, in chromosome and gene mapping, and in generating
XX antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
XX This sequence encodes a novel human secreted and transmembrane PRO
XX polypeptide
XX
XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores: 6.04e-52 Length: 713
Pred. No.: 462.00 Matches: 90
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
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Db 92 ATGACATTTTCTGTCTCACTATTATTGTTGGTATGTGAAGCTATTGGAGATCCAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
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Db 332 GCTCGGGCAGGGGTGTAAGAAACACT 361
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XX AC ABX90341;
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XX DT 01-MAY-2003 (first entry)
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XX DE Human secreted/transmembrane protein cDNA, #154.
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XX KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
XX KW pharmaceutical; diagnostic; therapeutic; gene therapy.
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XX OS Homo sapiens.
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XX PN US2002160384-A1.
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XX PD 31-OCT-2002.
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XX 14-NOV-2001; 2001US-00992598.
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XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
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PR	20-DEC-1999;	99WO-US030999

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PR 30-DEC-1999; 99WO-US0311243.
PR 30-DEC-1999; 99WO-US0311274.
PR 05-JAN-2000; 2000WO-US0002179.
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PR 11-FEB-2000; 2000WO-US0003776.
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PR 18-FEB-2000; 2000WO-US004342.
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PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX (GETH ) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
XX WPI; 2003-352836/33.
DR P-PSDB; ABU81106.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
XX Claim 2; Fig 473; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA6994-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
XX site at seqdata.uspto.gov/psipdsDIDEntry.html
XX
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Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ACA67230 (1-713)
QY 1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
Db 92 ATGACATTTTCTGTCTACATTTATTATTATTGTTGGTAAGTGAAGCTATTGGAGATCCAAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACACACAGT 211
QY 41 GlnProThrClnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACAAATCATCTTTTAGAAGACAGTGTGACTCTTACCACAAAGCTGTCAAAACCA 271
QY 61 GlyLysGlyTleValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyAlaGlu 80
Db 272 GGCAGGGCAGTATTAAGACAGGAATCTTGACTCAGAGGGGTATATTCTTGTGTGTGAA 331
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90

Db 332 GCCTGGGCGAGGGTGTAAAGAAAACACT 361
RESULT 13
ACA64409
ID ACA64409 standard; cDNA; 713 BP.
XX ACA64409;
AC ACA64409;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1159 cDNA.
XX
XX Human; secreted and transmembrane protein; cytostatic; anti-HIV;
XX virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
XX PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
XX drug screening; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-00989734.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0065770P.
XX 25-FEB-1998; 98US-0075945P.
XX 28-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088824P.
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XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089532P.
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XX 17-JUN-1998; 98US-0089598P.
XX 17-JUN-1998; 98US-0089599P.
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 18-JUN-1998; 98US-0089907P.
 18-JUN-1998; 98US-0089908P.
 16-SEP-1998; 98WO-US019330.
 17-SEP-1998; 98WO-US019437.
 17-SEP-1998; 98WO-US021141.
 01-DEC-1998; 98WO-US025108.
 05-JAN-1999; 99WO-US000106.
 08-MAR-1999; 99WO-US005028.
 02-JUN-1999; 99WO-US012252.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 01-DEC-1999; 99WO-US028634.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 22-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US004914.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005641.
 10-MAR-2000; 2000WO-US006319.
 15-MAR-2000; 2000WO-US006884.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 28-AUG-2001; 2001US-00941992.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski FJ;
 Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 Zhang Z;
 WPI; 2003-352829/33.
 P-FSDB; ABU72562.
 New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
 PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
 sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
 disease.
 Claim 1; Fig 271; 663pp; English.
 The invention describes a new isolated nucleic acid molecule comprising
 the full length coding sequence of the DNA deposited with the American
 Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
 encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
 useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These

are particularly useful for detecting or treating e.g. malignancies or
 cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
 leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
 disease in mammals. The PRO polypeptides are useful in drug screening,
 particularly as targets for therapeutic intervention in these diseases,
 and in the diagnostic determination of the presence of these diseases.
 The PRO polypeptides are also useful as molecular weight markers, or for
 chromosome identification. The PRO genes are useful as hybridisation
 probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
 The PRO genes may also be used in gene therapy, particularly for
 replacing a defective gene. This sequence encodes a novel human secreted
 and transmembrane PRO polypeptide

SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,04e-52 Length: 713
 Score: 462.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ACA64409 (1-713)

Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTyrArgSerAsn 20
 Db 92 ATGACATTTTTCGTCATATATATTATTGTTGGTATGTGAAGCTATTGGAGATCCAAT 151
 Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
 Db 152 TCAGGAAGCAACACATTTGAGATGGCTACTTCTTATCAAGAAATAAGAGAACACACAGT 211
 Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
 Db 212 CAACCCACACATCATCTTTAGAACACAGTGTGACTCTTACCACCAAGCTGTCAAAACCCACA 271
 Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
 Db 272 GGCAGGGCATATTAAAGACCGAATCTTGACTCAAGAGGGTTAATCTTGGTGCTGAA 331
 Qy 81 AlaTyrGlyArgGlyValLysLysAsnThr 90
 Db 332 GCCTGGGGCAGGGGTGTAAAGAAAAACACT 361

RESULT 14

ACA03839
 ID ACA03839 standard; cDNA; 713 BP.

AC ACA03839;

XX 23-MAY-2003 (first entry)

DE cDNA encoding human PRO polypeptide #237.

XX Human; PRO polypeptide; secreted and transmembrane protein;

XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

XX differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;

XX ss.

OS Homo sapiens.

XX US2003036180-A1.

XX 20-FEB-2003.

XX 09-MAY-2002; 2002US-00143114.

XX 31-MAR-1997; 97WO-US005230.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.

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PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 29-OCT-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012232.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 04-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00786498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR P-ESDE; ABU66806.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
XX Claim 2; Fig 473; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ACA03839 (1-713)
QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTtpArgSerAsn 20
DB 92 ATGACATTTTTCCTGCTACTATATATTGTTGGTATGTGAGCTATTTGGAGATCCAAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
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Db      152 TCAGGAAGCAACACATTGGAGATGGCTACTTTCTATCAGAAATATAAGAGAACCAAGT 211
Qy      41  GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db      212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCA 271
Qy      61  GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyValaGlu 80
Db      272 GGCAGGGGCATAGTTAAAGACGGAATCTTGACTCAAGAGGTTAATCTTGTTGCTGAA 331
Qy      81  AlaTrpGlyArgGlyValLysLysAsnThr 90
Db      332 GCCTGGGGCAGGGGTGAAGAAAAACAACACT 361

RESULT 15
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ID      ABX89377 standard; cDNA; 713 BP.
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AC      ABX89377;
XX
DT      13-MAY-2003 (first entry)
XX
DE      DNA encoding novel secreted and transmembrane protein PRO1159.
XX
KW      Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW      cardiac insufficiency disorder; cancer; tumour; immune response;
KW      adrenal cortical capillary endothelial growth; c-fos induction;
KW      vascular endothelial growth factor inhibition; VEGF inhibition;
KW      endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW      retinal neurons cell survival; rod photoreceptor cell survival;
KW      retinal disorder; retinitis pigmentosa; kidney disorder;
KW      mammalian kidney mesangial cell proliferation; Berger disease;
KW      dermatitis; herpetic keratitis; Crohn's disease; chondrocyte proliferation;
KW      chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS      Homo sapiens.
XX
XX
XX      US2003017563-A1.
XX
PD      23-JAN-2003.
XX
XX
XX      07-MAY-2002; 2002US-00140808.
XX
XX      31-MAR-1997; 97WO-US005230.
XX      12-JUN-1998; 98WO-US012456.
XX      14-JUL-1998; 98WO-US014552.
XX      28-AUG-1998; 98WO-US017888.
XX      10-SEP-1998; 98WO-US018824.
XX      14-SEP-1998; 98WO-US019094.
XX      14-SEP-1998; 98WO-US019177.
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XX      29-OCT-1998; 98WO-US022992.
XX      20-NOV-1998; 98WO-US024855.
XX      01-DEC-1998; 98WO-US025108.
XX      05-JAN-1999; 99WO-US000106.
XX      08-MAR-1999; 99WO-US005028.
XX      10-MAR-1999; 99WO-US005190.
XX      20-APR-1999; 99WO-US008615.
XX      14-MAY-1999; 99WO-US010733.
XX      02-JUN-1999; 99WO-US012252.
XX      01-SEP-1999; 99WO-US020111.
XX      08-SEP-1999; 99WO-US020594.
XX      13-SEP-1999; 99WO-US020944.
XX      15-SEP-1999; 99WO-US021090.
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XX      30-NOV-1999; 99WO-US028313.
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XX      01-DEC-1999; 99WO-US028301.
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XX      02-DEC-1999; 99WO-US028564.
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XX      20-DEC-1999; 99WO-US030911.
XX      20-DEC-1999; 99WO-US030999.
XX      22-DEC-1999; 99WO-US030720.
XX      30-DEC-1999; 99WO-US031243.
XX      05-JAN-2000; 99WO-US031274.
XX      06-JAN-2000; 2000WO-US000219.
XX      06-JAN-2000; 2000WO-US000277.
XX      11-FEB-2000; 2000WO-US000376.
XX      11-FEB-2000; 2000WO-US0003565.
XX      18-FEB-2000; 2000WO-US0004341.
XX      18-FEB-2000; 2000WO-US0004342.
XX      22-FEB-2000; 2000WO-US0004414.
XX      24-FEB-2000; 2000WO-US0004914.
XX      24-FEB-2000; 2000WO-US005004.
XX      01-MAR-2000; 2000WO-US005601.
XX      02-MAR-2000; 2000WO-US005746.
XX      02-MAR-2000; 2000WO-US005841.
XX      10-MAR-2000; 2000WO-US006319.
XX      15-MAR-2000; 2000WO-US006884.
XX      20-MAR-2000; 2000WO-US007377.
XX      21-MAR-2000; 2000WO-US007532.
XX      30-MAR-2000; 2000WO-US008439.
XX      17-MAY-2000; 2000WO-US013705.
XX      22-MAY-2000; 2000WO-US014042.
XX      30-MAY-2000; 2000WO-US014941.
XX      02-JUN-2000; 2000WO-US015264.
XX      28-JUL-2000; 2000WO-US020710.
XX      11-AUG-2000; 2000WO-US022031.
XX      23-AUG-2000; 2000WO-US023522.
XX      24-AUG-2000; 2000WO-US023328.
XX      08-NOV-2000; 2000WO-US030952.
XX      10-NOV-2000; 2000WO-US030873.
XX      01-DEC-2000; 2000WO-US032878.
XX      20-DEC-2000; 2000US-00747259.
XX      20-DEC-2000; 2000WO-US034956.
XX      28-FEB-2001; 2001US-00796498.
XX      01-MAR-2001; 2001WO-US006520.
XX      09-MAR-2001; 2001WO-US006566.
XX      14-MAR-2001; 2001US-00802706.
XX      22-MAR-2001; 2001US-00808689.
XX      05-APR-2001; 2001US-00828366.
XX      10-MAY-2001; 2001US-00854208.
XX      18-MAY-2001; 2001US-00860216.
XX      25-MAY-2001; 2001US-00866028.
XX      25-MAY-2001; 2001US-00866034.
XX      01-JUN-2001; 2001US-00872035.
XX      05-JUN-2001; 2001WO-US017800.
XX      14-JUN-2001; 2001US-00882536.
XX      19-JUN-2001; 2001US-00886342.
XX      20-JUN-2001; 2001WO-US019692.
XX      21-JUN-2001; 2001US-00887879.
XX      22-JUN-2001; 2001WO-US020116.
XX      29-JUN-2001; 2001WO-US021066.
XX      09-JUL-2001; 2001WO-US021735.
XX      18-JUL-2001; 2001US-00908827.
XX      06-AUG-2001; 2001US-00924419.
XX      09-AUG-2001; 2001US-00927796.
XX      16-AUG-2001; 2001US-00931836.
XX      19-DEC-2001; 2001US-00028072.
XX
XX      (GETH ) GENENTECH INC.
XX
XX
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PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.
DR P-PSDB; ABUS9887.
XX
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
XX
PS Claim 2; Fig 473; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX
XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
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Score: 462.00 Matches: 90
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DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ABX89377 (1-713)

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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGCTGTCAAAACACACA 271
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Db 332 GCCTGGGGCAGGGGTCTTAAAGAAAAACACT 361
Search completed: April 4, 2004, 08:12:56
Job time : 433 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2004, 07:01:32 ; Search time 3358 Seconds
(without alignments)
1161.666 Million cell updates/sec

Title: US-09-989-293A-377
Perfect score: 462
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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34: em_hcg_pln.*
35: em_hcg_rod.*
36: em_hcg_man.*
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38: em_sy.*
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41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	462	100.0	713	6	AR252626	Sequence
2	462	100.0	713	6	AX055452	Sequence
3	462	100.0	713	6	AX403489	Sequence
4	462	100.0	713	6	AX464340	Sequence
5	462	100.0	713	9	AY358685	Homo sapi
6	462	100.0	165414	9	AC024224	Homo sapi
7	369	79.9	240864	2	AC006510	Homo sapi
8	247.5	53.6	741	6	E21012	Novel membr
9	247.5	53.6	744	9	AF400595	Homo sapi
10	247.5	53.6	744	9	AF026769	Homo sapi
11	247.5	53.6	787	9	AF400601	Homo sapi
12	247.5	53.6	1018	6	BD136999	Isolated
13	247.5	53.6	1153	6	AX664609	Sequence
14	247.5	53.6	1153	9	HS312373	Homo sapi
15	247.5	53.6	1606	9	AF313468	Homo sapi
16	247.5	53.0	881	9	AF400602	Homo sapi
17	245	51.1	534	6	E21014	Novel membr
18	236	47.1	744	9	AF508729	Macaca mu
19	217.5	45.0	221471	2	AC138620	Mus muscu
20	208	39.9	273867	2	AC112033	Rattus no
21	184.5	31.1	2298	6	BD056525	Unigue de
22	143.5	31.1	2298	10	AF262985	Mus muscu
23	143.5	30.2	528	6	BD056528	Unigue de
24	139.5	29.5	1329	10	BC027742	Mus muscu
25	136.5	26.4	85	6	AX912349	Sequence
26	122	26.4	85	6	BD047882	Sequence
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28	86.5	18.7	211342	2	AC113877	Rattus no
29	86.5	18.7	220557	2	AC111741	Rattus no
30	85	18.4	237031	2	AC128368	Rattus no
31	85	18.4	235295	2	AC126817	Rattus no
32	83	18.0	110041	2	AC141026	Rattus no
33	83	18.0	231264	2	AC095739	Rattus no
34	83	18.0	244024	2	AC133293	Rattus no
35	82.5	17.9	233440	2	AC094560	Rattus no
36	81.5	17.6	10255	1	AE009926	Pyrobacul
37	81	17.5	254951	2	AC122999	Rattus no
38	80	17.3	11193	1	AE010087	Streptoco
39	80	17.3	43106	7	AY050245	Streptoco
40	80	17.3	51908	1	AE014160	Streptoco
41	80	17.3	163309	2	AC116727	Mus muscu
42	80	17.3	244024	2	AC133293	Rattus no
43	80	17.3	288358	2	AC106121	Rattus no
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ALIGNMENTS

RESULT 1

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Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-989-293A-377 (1-90) x AX055452 (1-713)

Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTPrArgSerAsn 20
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Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGAGACACACATTCGAGATGGCTACTTCTTCTATCAAGAATAAAGAGAACCCAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCAC 271
Qy 61 GlyLysGlyTLeValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
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Qy 81 AlaTPrGlyArgGlyValLysLysAsnThr 90
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RESULT 3
LOCUS AX403489 713 bp DNA linear PAT 14-JUN-2000
DEFINITION Sequence 376 from Patent WO0073454.
ACCESSION AX403489
VERSION AX403489.1 GI:21436980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Gimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Pooni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 376 07-DEC-2000;
Genentech Inc. (US)
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Location/Qualifiers
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Alignment Scores:
Pred. No.: 6,45e-44 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
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US-09-989-293A-377 (1-90) x AX403489 (1-713)

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Db 152 TCAGGAAGCAACACATGAGAAATGGCTACTTCTATCAAGAAATAAAGAGAACACACAT 211
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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
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QY 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyAlaGlu 80
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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
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Db 332 GCCTGGGCGAGGGGTAAAGAAAAACACT 361
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RESULT 4
AX464340

LOCUS AX464340 713 bp DNA linear PAT 16-JUN-2002

DEFINITION Sequence 473 from Patent WO0140466.

ACCESSION AX464340

VERSION AX464340.1 GI:21899186

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same

JOURNAL Patent: WO 0140466-A 473 07-JUN-2001; Genentech Inc. (US)

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Db 332 GCCTGGGCGAGGGGTAAAGAAAAACACT 361

RESULT 5
AY358685

LOCUS AY358685 713 bp mRNA linear PRI 03-OCT-2003

DEFINITION Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.

ACCESSION AY358685

VERSION AY358685.1 GI:37182491

KEYWORDS FLI CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 713)

AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, O., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.L. and Godowski, P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)

PUBMED 12975309

REFERENCE 2 (bases 1 to 713)

AUTHORS Clark, H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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ORIGIN

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Score: 462.00 Matches: 90
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US-09-989-293A-377 (1-90) x AY358685 (1-713)

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RESULT 6
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 DEFINITION Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute
 Human PAC Library) complete sequence.
 ACCESSION AC024224
 VERSION AC024224.33 GI:21240476
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 165414)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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 Lien,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
 Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
 Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
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 Nguyen,N., Nickerson,E., Nwokwenkwo,S., Oguh,M., Okwuonu,G.,
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 Peters,L., Pickens,R., Primus,E., Fu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojupokan,I., Rolfe,M., Ruiz,S., Savery,G.,
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 Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucheraipati,R.,
 Weinstock,G. and Gibbs,R.

Direct Submission
 Unpublished
 2 (bases 1 to 165414)
 Worley,K.C.
 Direct Submission
 Submitted (28-FEB-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 165414)

REFERENCE
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 AUTHORS
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AUTHORS
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 JOURNAL
 COMMENT

Worley,K.C.
 Direct Submission
 Submitted (26-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 165414)
 Worley,K.C.
 Direct Submission
 Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 29, 2002 this sequence version replaced gi:21206012.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:
 STSs are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
 EST and cDNA sequences. Genes demonstrate at least two exons
 flanked by consensus splice sites that maintained sequence
 continuity across the splice junctions. Sequences that are not
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
 standard of Double strand coverage with a minimum of 2 clones and 2
 reads with no ambiguities or 2 chemistries with a minimum of 2
 clones and 3 reads with no ambiguities. If the sequence quality for
 a region does not meet this standard, it will be indicated in the
 annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
 standards - estimated error rate less than 1 per 10,000 bases.
 Reports of lowest quality individual bases and measures of base
 quality are listed below. Description of the metrics can be found
 at [URL](http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html).

QUALSTAT-REPORT.
 Location/Qualifiers
 1. .165414
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 /chromosome="12"
 /clone="RP11-133L14"
 /complement(482..533)
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 717..777
 /rpt_family="(TC)n"
 754..774
 /note="Variable size of homopolymeric repeat in subclones"
 /function="unresolved homopolymeric run"
 778..814
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 /complement(2040..2134)
 /rpt_family="MIR"
 /complement(2987..3137)
 /rpt_family="L1PA3"
 /complement(4558..4629)
 /rpt_family="MER5A"
 4859..4941

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 misc_feature
 repeat_region
 repeat_region
 repeat_region
 repeat_region
 repeat_region

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/rpt_family="AT_rich"
6420_..6491
/rpt_family="Charlie2"
complement(6577_..6703)
/rpt_family="MIR"
6766_..6966
/rpt_family="Charlie2"
6980_..7102
/rpt_family="Charlie2"
7137_..7184
/rpt_family="AT_rich"
complement(7215_..7505)
/rpt_family="L1MA4"
8677_..8904
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/rpt_family="Aluub"
11416_..11839
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19837_..19882
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-09-989-293A-377 (1-90) x AC024224 (1-165414)
QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTTPArgSerAen 20
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QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 117268 TCAGGAAGCAACACATTTGGAGATGGCTACTTCTATCAGAAATAAGAGACACACACT 117209
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 117208 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGAGCTGTCAAAACCA 117149
QY 61 GlyLysGlyLleValLysGlyArgAsnLeuAspSerArgGlyLeuLleuGluAlaGlu 80
Db 117148 GGCNAAGGGCATAAGTTAAAGGACGGAATCTTGACTCAAGAGGTTAATTTCTTGCTGTA 117089
QY 81 AlaTTPGlyArgGlyValLysLysAsnThr 90
Db 117088 GCTGGGGCAGGGGTGTAAGAAACACT 117059

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RESULT 7
AC006510/c
LOCUS

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DEFINITION Homo sapiens clone RP11-13C13, RP11-656E20, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
AC006510 AC006514
VERSION AC006510.8 GI:10122018
HTG: HTGS PHASE1.
SOURCE Homo sapiens (human)

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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 240864)

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REFERENCE
AUTHORS

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C., Alsbrooks, S.L., Amaral, H.C., Are, J.R., Banks, T., Barbara, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Homs, Z., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, I., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Liu, C., Liu, J., Liu, W., Louseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokkenwo, S., Oguh, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshkari, N., Sisson, I., Sodergren, E., Sotaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, R., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,

Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
and Gibbs R.
Direct Submission
2 (bases 1 to 240864)
Worley,K.C.
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2000 this sequence version replaced gi:10086352.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: J-33
Center clone name: RP11-13C13, RP11-656E20
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 23% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71594 bases at least Q40
Consensus quality: 93014 bases at least Q30
Consensus quality: 110702 bases at least Q20
Estimated insert size: 229041; sum-of-contigs estimation
Estimated insert size: 331000; agarose-fp estimation
Quality coverage: 0.6x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 11085: contig of 11085 bp in length
11185: gap of unknown length
134782: contig of 23597 bp in length
134783: gap of unknown length
134883: contig of 28772 bp in length
163654: gap of unknown length
163754: gap of unknown length
163755: contig of 21296 bp in length
185051: gap of unknown length
185151: contig of 9652 bp in length
194803: gap of unknown length
202527: contig of 7625 bp in length
202628: gap of unknown length
202628: contig of 6031 bp in length
208659: gap of unknown length
208759: contig of 13027 bp in length
221785: gap of unknown length
230142: contig of 8257 bp in length
230243: gap of unknown length
232626: gap of unknown length
232726: gap of unknown length
234459: contig of 1734 bp in length
234460: gap of unknown length
234559: gap of unknown length
235821: contig of 1262 bp in length
235822: gap of unknown length
235921: gap of unknown length
237146: contig of 1225 bp in length
237147: gap of unknown length
237247: contig of 1171 bp in length
238418: gap of unknown length
238518: gap of unknown length
239649: contig of 1132 bp in length
239749: gap of unknown length
240864: contig of 1115 bp in length.

FEATURES source

Location/Qualifiers
1. .240864
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-13C13, RP11-656E20"

ORIGIN

Alignment Scores:
Pred. No.: 1.61e-30 Length: 240864
Score: 269.00 Matches: 87
Percent Similarity: 90.62% Conservatives: 0
Best Local Similarity: 90.62% Mismatches: 3
Query Match: 79.87% Indels: 6
DB: 2 Gaps: 0

US-09-989-293A-377 (1-90) x AC006510 (1-240864)

QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTTPArgSerAen 20
Db 211659 ATGACATTTTCTGTCTCACTATTATTATTGGTATGTGAAGCTATTGGAGATCCAAAT 211600
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyr-PheLeuSerArgAsnLysGluAenHis 40
Db 211599 TCAGGAAGCACACATTTGGAGATGGCTACTTCTTTCACAGAAATAAGAGAACACAG 211540
QY 40 r-GlnProThrGlnSerSerLeuGluAenSerValThrProThr-LysAlaValLysThr 59
Db 211539 TCCACCCACACATTTCTTTAGAGACAGTGTACTCTACCAAAAGCTGTCAAAACC 211480
QY 60 Thr-GlyLysGlyLeValLys-GlyArgAsnLeuAspSer-ArgGlyLeuLeuLeuGly 78
Db 211479 ACCGAGCAAGGCATAGTTTAAACAGACGGAATCTTGACTCAAGAGGGTTAATCTTGT 211420
QY 79 AlaGluAlaIleTTPArgGlyValLysLysAsnThr 90
Db 211419 GCTGAGCTGGGGCAGGGGTGTAAAGAAACACT 211384

RESULT 8 AF400597 LOCUS

DEFINITION Homo sapiens beta-glucan receptor isoform C (BGR) mRNA, complete cds, alternatively spliced.
AF400597 625 bp mRNA linear PRI 19-NOV-2001
VERSION AF400597.1 GI:15936703

KEYWORDS SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 625)
Willment,J.A., Gordon,S. and Brown,G.D.
Characterization of the human beta -glucan receptor and its
alternatively spliced isoforms

JOURNAL MEDLINE

J Biol. Chem. 276 (47), 43818-43823 (2001)
21570237
PUBMED 11567029

REFERENCE AUTHORS

2 (bases 1 to 625)
Willment,J.A., Gordon,S. and Brown,G.D.
Direct Submission
Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK

JOURNAL TITLE

Oxford University, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers
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FEATURES source

1. .625
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/tissue_type="peripheral blood leukocyte"
1. .625
/gene="BGR"
1. .570

gene CDS

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1; alternatively spliced"
/codon_start=1
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ORIGIN

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Alignment Scores:
Pred. No.: 3,26e-19 Length: 625
Score: 247.50 Matches: 50
Percent Similarity: 87.10% Conservatve: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 9 Gaps: 1
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US-09-989-293A-377 (1-90) x AF400597 (1-625)

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QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTTPArgSer 19
Db 157 CTATGCTTGGTAATACCTGGTATAGCTGGTCTCTGGTACCATGGCTATTGGAGATCC 216
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 217 AATTCAGGAGCAACACATTCGGAATGGCTATCTTCTATCAAGAAATAAGAGAACCC 276
QY 40 SerGlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACC 336
QY 60 ThrGly 61
Db 337 ACAGGG 342
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RESULT 9

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LOCUS Novel membrane protein and DNA thereof. 741 bp DNA linear PAT 18-JUN-2001
DEFINITION
ACCESSION E21012
VERSION E21012.1 GI:13023572
KEYWORDS JP 1999001497-A/2.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 741)
AUTHORS Shuji.H., Shoji.F., Kazunori.N. and Yasushi.A.
TITLE Novel membrane protein and DNA thereof
JOURNAL Patent: JP 1999001497-A 2 06-JAN-1999;
COMMENT TAKEDA CHEM IND LTD
OS Unidentified
PN JP 1999001497-A/2
PD 06-JAN-1999
PF 13-JUN-1997 JP 1997156376
PR
PI SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, YASUSHI ARAVA PC
C07K14/47, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, PC
A61K39/395,
PC A61K48/00, C07K16/28, C12N1/21, C12N15/09, C12P21/02, C12Q1/68, PC
G01N33/53//
PC (C12N1/21, C12R1:19), (C12N15/09, C12R1:91), A61K37/02, A61K37/02,
PC A61K37/02,
PC A61K37/02, A61K37/02, C12N15/00, (C12N15/00, C12R1:91) CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..741
FT /organism='Unidentified'.
FT Location/Qualifiers
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source

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ORIGIN

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Alignment Scores:
Pred. No.: 3,9e-19 Length: 741
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Percent Similarity: 87.10% Conservatve: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 6 Gaps: 1
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US-09-989-293A-377 (1-90) x E21012 (1-741)

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QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTTPArgSer 19
Db 157 CTATGCTTGGTAATACCTGGTATAGCTGGTCTCTGGTACCATGGCTATTGGAGATCC 216
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 217 AATTCAGGAGCAACACATTCGGAATGGCTATCTTCTATCAAGAAATAAGAGAACCC 276
QY 40 SerGlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACC 336
QY 60 ThrGly 61
Db 337 ACAGGG 342
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RESULT 10

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AF400595
LOCUS Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete cds, alternatively spliced. 744 bp mRNA linear PRI 19-NOV-2001
DEFINITION
ACCESSION AF400595
VERSION AF400595.1 GI:15986699
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
MEDLINE 21570237
PUBMED 11567029
REFERENCE 2 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology, Oxford University, South Parks Road, Oxford OX1 3RE, UK
FEATURES
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1; alternatively spliced"
/codon_start=1
/product="beta-glucan receptor isoform A"
/protein_id="AAL11711.1"
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ORIGIN

Alignment Scores: 3.92e-19 Length: 744
 Pred. No.: 247.50 Matches: 50
 Score: 247.50
 Percent Similarity: 87.10% Conservative: 4
 Best Local Similarity: 80.65% Mismatches: 3
 Query Match: 53.57% Indels: 5
 DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x AF400595 (1-744)

QY 5 LeuSerLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19
 Db 157 CTATGCTTGGTAATACCTGGTGTGCTCTGGGTACCATGGCTATTGGAGATCC 216
 QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
 Db 217 AATTGAGGAAGCAACATCGAGATGGCTACTTTCTATCAAGAAATAAAGAACCCAC 276
 QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
 Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGGTGTCAAACC 336
 QY 60 ThrGly 61
 Db 337 ACAGGG 342

RESULT 11

AY026769 744 bp mRNA linear PRI 05-OCT-2001
 LOCUS
 DEFINITION Homo sapiens lectin-like receptor 1 (DECTIN1) mRNA, complete cds.

ACCESSION AY026769
 VERSION AY026769.2 GI:15967096

KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 744)
 Hernandez-Falcon, P., Arce, I., Roda-Navarro, P. and Fernandez-Ruiz, E.

Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
 expressed on dendritic cells

Immunogenetics 53 (4), 288-295 (2001)

21383615

PUBMED 11491532

REFERENCE 2 (bases 1 to 744)

Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.

AUTHORS

TITLE

Submitted (01-FEB-2001) Biologia Molecular, Hospital de la

Princesa, Diego de Leon 62, Madrid 28006, Spain

3 (bases 1 to 744)

Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.

AUTHORS

TITLE

Submitted (05-OCT-2001) Biologia Molecular, Hospital de la

Princesa, Diego de Leon 62, Madrid 28006, Spain

Sequence update by submitter

On Oct 5, 2001 this sequence version replaced gi:14278818.

REMARK

COMMENT

FEATURES

source

gene

CDS

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 SVTPKAVKTVGLSPCPNNWIIYEKSYLFSMSLNSWDGSKRCQWQLGSNLLKIDS
 SNELGFIKQVSSQPDNSFWIGLSRPQTEVPLWEDGSTFSSNLFQIRTTATQENPSP
 NCWTHVSVIYDQLCSVPSYSICEKFSM"

ORIGIN

Alignment Scores: 3.92e-19 Length: 744
 Pred. No.: 247.50 Matches: 50
 Score: 247.50
 Percent Similarity: 87.10% Conservative: 4
 Best Local Similarity: 80.65% Mismatches: 3
 Query Match: 53.57% Indels: 5
 DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x AY026769 (1-744)

QY 5 LeuSerLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19
 Db 157 CTATGCTTGGTAATACCTGGTGTGCTCTGGGTACCATGGCTATTGGAGATCC 216
 QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
 Db 217 AATTGAGGAAGCAACATCGAGATGGCTACTTTCTATCAAGAAATAAAGAACCCAC 276
 QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
 Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGGTGTCAAACC 336
 QY 60 ThrGly 61
 Db 337 ACAGGG 342

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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/ gene="BGR"
/ note="C-type lectin BGRG; alternatively spliced"
/ codon_start=1
/ product="beta-glucan receptor isoform G"
/ protein_id="AAL1171.1"
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LIAVILGICLVILVIAVLGTWAIWRNSGNTLENGYFLSRNKHNSQPTQSSLED
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ORIGIN

Alignment Scores:
Pred. No.: 4,16e-19 Length: 787
Score: 247.50 Matches: 50
Percent Similarity: 87.10% Conservative: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: Gaps: 1

US-09-989-293A-377 (1-90) x AF400601 (1-787)

QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTpaArgSer 19
Db 157 CTATGCTTGTAATACATGGTATGCTGCTGCTGCTGCTATTTGGAGATCC 216
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 217 AATCAGGAGCACACATTTGGAGATGGCTACTTTCTATCAGAATAAAGAGACCAC 276
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 277 AGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTCTCTACCAAGCTGTCAAACC 336
QY 60 ThrGly 61
Db 337 ACAGGG 342

RESULT 13
BD136999
LOCUS BD136999 1018 bp DNA linear PAT 18-SEP-2002
DEFINITION Isolated mammalian membrane protein gene and reagent relating
thereto.
ACCESSION BD136999
VERSION BD136999.1 GI:23231944
KEYWORDS JP 2002506645-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1018)
Chalus, L., Quan, A., Bates, E.E.M., Gorman, D.M., Saeland, S.,
Lebecque, S.J.E. and Jr, J.H.P.
Isolated mammalian membrane protein gene and reagent relating
Patent: JP 2002506645-A 05-MAR-2002;
SCHERING CORP
OS Homo sapiens (human)
PN JP 2002506645-A/3
PD 05-MAR-2002
PF 16-MAR-1999 JP 2000536856
PR 17-MAR-1998 US 09/040111
PI LIONEL CHALUS, AHN QUAN, ELIZABETH ESTHER MARY BATES, DANIEL M
GORMAN,
PI SEM SAE LAND, SERGE J E LEBECQUE, JOSEPH H PHILIPPS JR, PC
C12N15/09, A61K31/70, A61K38/00, A61K39/395, A61K39/395, A61F35/00, PC
A61P37/02,
PC A61P43/00, C07K14/705, C07K16/28, C12N1/19, C12N1/21, C12N5/10, PC
C12Q1/68.
PC G01N33/68, C12N15/00, A61K37/02, C12N5/00
CC Isolated mammalian membrane protein gene and reagent relating
thereto.
CC Key Location/Qualifiers
FH CDS (150)..(900).
FT CDS

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QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
DB 372 AATTGAGGAGCAACACATGAGTGGTACTTCTTCAAGAAATPAGAGAACAC 431
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
DB 432 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGCTGTCAAAACC 491
QY 60 ThrGly 61
DB 492 ACAGGG 497

RESULT 15
HSA312373
LOCUS HSA312373 1153 bp mRNA linear PRI 03-JUL-2001
DEFINITION Homo sapiens mRNA for DECTIN-1 receptor, splice variant 2.
ACCESSION AJ312373
VERSION AJ312373.1 GI:14599395
KEYWORDS alternative splicing; C-type lectin-1; DECTIN-1 gene; DECTIN-1
receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sobanov Y., Bernreiter A., Derdak S., Mechtcheriakova D.,
Duechler M., Kalthoff F. and Hofer E.
TITLE A novel cluster of lectin-like receptor genes expressed in
monocytic, dendritic and endothelial cells maps close to the NK
receptor genes in the human NK gene complex
Unpublished
2 (bases 1 to 1153)
Sobanov Y.
Direct Submission
Submitted (02-JUL-2001) Vascular Biology and Thrombosis Research,
University of Vienna, Brunnerstrasse 59, Vienna A-1235, Austria
COMMENT Alternative splicing: See also AJ312372.
FEATURES
source
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/db_xref="taxon:9606"
/chromosome="12"
/map="12p12.3-p13.2"
/clone="AI741964"
/notes="NK gene complex, between CLEC-1 and LOX-1 genes"
1..1153
/gene="DECTIN-1"
156..899
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LIAVLGLCLVILVIAVLGTMALWRSNGSNTLENGYFLSRNKHNSQPTQSSLED
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SNEIGFTVQVSSQFDNSFWTGLSRQTEVFWEDGTFSSNLFQIRTTATQENPSP
NCVWIHVSIVYDQLCVSPSYSCIKKFSM"

ORIGIN
Alignment Scores:
Pred. No.: 6,22e-19 Length: 1153
Score: 247.50 Matches: 50
Percent Similarity: 87.10% Conservative: 4
Best Local Similarity: 80.65% Mismatches: 3
Query Match: 53.57% Indels: 5
DB: 9 Gaps: 1
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US-09-989-293A-377 (1-90) x HSA312373 (1-1153)
QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTIpArgSer 19
DB 312 CTATGCTTGGTAATACTGGTGATAGCTGTGCTCGGTACCATGGCTATTGGAGATCC 371
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
DB 372 AATTGAGGAGCAACACATGAGTGGTACTTCTTCAAGAAATPAGAGAACAC 431
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
DB 432 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGCTGTCAAAACC 491
QY 60 ThrGly 61
DB 492 ACAGGG 497

Search completed: April 4, 2004, 09:09:38
Job time : 3398 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 4, 2004, 07:56:38 ; Search time 2701 Seconds
(without alignments)
995.037 Million cell updates/sec

Title: US-09-989-293A-377
Perfect score: 462
Sequence: 1 MTFLLSLLLLVCEAIWRSN.....DSRGLILGAERAGGVKKNT 90

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2_1/USPTO.spool/US09989293/runat_31032004_081503_14843/app_query.fasta_1.263
-DB=EST -QFMT=fastcap -SUFFIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09989293 @CGN 1_1906 @runat_31032004_081503_14843 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	365.5	79.1	663	9	AU185777	AU185777 AU185777
C 2	306	66.2	800	14	CB958894	CB958894 AGENCOURT
C 3	247.5	53.6	659	12	BI018962	BI018962 IL3-MT026
C 4	209	45.2	663	28	AZ121459	AZ121459 RPL1-23-3
C 5	206	44.6	673	9	AV721179	AV721179 AV721179
C 6	174	37.7	582	14	CB420818	CB420818 593806 MA
C 7	138.5	30.0	855	12	BI107684	BI107684 602891529
C 8	82	17.7	833	10	BE865626	BE865626 601677978
C 9	82	17.7	924	12	BG165693	BG165693 602344512
C 10	81	17.5	1121	29	CNS04830	AL290421 Tetraodon
C 11	80.5	17.4	683	12	BI914658	BI914658 603179440
C 12	79	17.1	391	28	BH354332	BH354332 CH230-163
C 13	79	17.1	504	28	BH354326	BH354326 CH230-163
C 14	79	17.1	536	12	BJ193507	BJ193507 BJ193507
C 15	79	17.1	644	13	BQ406117	BQ406117 GA_Rd009
C 16	79	17.1	845	14	CF735257	CF735257 UT-M-HB0
C 17	78.5	17.0	884	29	CG183911	CG183911 PUCOT97TD
C 18	78.5	17.0	929	29	CG457562	CG457562 PUKF73TD
C 19	78	16.9	649	29	CC701258	CC701258 OGWHR80TV
C 20	78	16.9	653	28	CC11703	CC11703 ii73e02.g
C 21	78	16.9	679	29	CG691911	CG691911 ZMMBBb028
C 22	78	16.9	723	29	AG009588	AG009588 Homo sapi
C 23	78	16.9	819	29	CC616498	CC616498 OGUJF08TH
C 24	77	16.7	477	12	BG276251	BG276251 uv02b11.y
C 25	77	16.7	626	28	AZ822524	AZ822524 2M0095D21
C 26	77	16.7	943	13	BQ920084	BQ920084 AGENCOURT
C 27	77	16.7	967	28	B08136	B08136 F8C13-T7-1
C 28	77	16.7	1383	10	BF238075	BF238075 601811790
C 29	76.5	16.6	483	10	BE723365	BE723365 193059 MA
C 30	76.5	16.6	551	12	BI898668	BI898668 480374 MA
C 31	76.5	16.6	601	14	CB457947	CB457947 716067 MA
C 32	76.5	16.6	867	10	BF214995	BF214995 601847310
C 33	76	16.5	320	28	BH198757	BH198757 TC3-64015
C 34	76	16.5	781	13	BUS96994	BUS96994 AGENCOURT
C 35	76	16.5	968	28	BH135384	BH135384 ENTPA53TR
C 36	76	16.5	1007	29	CNS021MF	AL199104 Tetraodon
C 37	75.5	16.3	404	28	BH123205	BH123205 RPL1-24-2
C 38	75.5	16.3	504	9	AA614424	AA614424 nm89b06.s
C 39	75.5	16.3	774	12	BI553528	BI553528 601197519
C 40	75.5	16.3	879	13	BX346820	BX346820 BX346820
C 41	75.5	16.3	1006	13	BQ21671	BQ21671 AGENCOURT
C 42	75.5	16.3	1148	29	CG753752	CG753752 P048-4-H0
C 43	75	16.2	608	9	AV827009	AV827009 AV827009
C 44	75	16.2	672	29	CC615145	CC615145 OGVAG73TV
C 45	75	16.2	717	14	CF433331	CF433331 NIT1_26_G

ALIGNMENTS

RESULT 1
LOCUS AU185777/c
DEFINITION AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens
cDNA clone B02302-019, mRNA sequence.
ACCESSION AU185777
VERSION AU185777.1 GI:14623690
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)

AUTHORS Sugita, Y., Oshida, T. and Oya, Y.
 TITLE Human cDNA sequencing
 JOURNAL Unpublished (2001)
 COMMENT Contact: Yuji Sugita
 Genex Research, Inc.
 907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan
 Tel: 81-44-797-2281
 Fax: 81-44-797-2622
 Email: syuji@genex.co.jp, URL: http://www.genex.co.jp.

FEATURES
 source
 Location/Qualifiers
 1.663
 /organism="Homo sapiens"
 /mol_type="mRNA"
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ORIGIN

Alignment Scores:
 Pred. No.: 5.27e-36 Length: 663
 Score: 365.50 Matches: 81
 Percent Similarity: 89.01% Conservative: 0
 Best Local Similarity: 89.01% Mismatches: 8
 Query Match: 79.11% Indels: 3
 DB: 9 Gaps: 1

US-09-989-293a-377 (1-90) x AU185777 (1-663)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTTP-ArgSerAs 20
 Db 507 ATGACATTTTTCGTCACNATTATNATGTTGCTATGTAAGCTATTTGGNAGATCAA 448
 Qy 20 nSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 40
 Db 447 TTCAGNAGC---ACATTGNAAGATGGCTACTTTCTATCAAGAATAAAGAACACACAG 391
 Qy 40 rGlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThrTh 60
 Db 390 TCAACCCACACATTCATCTTTAGAGACAGTGG-ACCTCACCACAAAGCTGTCAAAACAC 332
 Qy 60 rGlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGl 80
 Db 331 AGGCAAGGGCAGTAGTTAAGACGGAATCTTGACTCAAGAGGGTTAATCTTGTGTGTA 272
 Qy 80 uAlaTrpGlyArgGlyValLysLysAsnThr 90
 Db 271 AGCCTGGGCGAGGGGTGTAAAGAAACAACT 241

RESULT 2
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 LOCUS AGENCOURT 13785021 NIH MGC 184 Homo sapiens cDNA clone
 DEFINITION IMAGE:30352338 5', mRNA sequence.
 CB958894
 ACCSSION CB958894.1 GI:30215010
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 800)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:

http://image.llnl.gov
 Plate: NDCM151 row: e column: 19
 High quality sequence stop: 488.

FEATURES

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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:30352338"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
 SfiI (ggcattatgcc); Site_2: SfiI (ggcgctcgcc);
 Library is oligo-dr primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCGCATATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 2.69e-28 Length: 800
 Score: 306.00 Matches: 70
 Percent Similarity: 66.38% Conservative: 7
 Best Local Similarity: 60.34% Mismatches: 10
 Query Match: 66.23% Indels: 29
 DB: 14 Gaps: 3

US-09-989-293a-377 (1-90) x CB958894 (1-800)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTTP-ArgSerAsn 20
 Db 342 ATGACATTTTCTGTCTACATTTATTATTCTGTGTATGTGAAGCTATTTGGAGATCCAAT 401
 Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
 Db 402 TCAGGAGACACACATTTGGAGAATGGCTACTTTCTATCAAGAAATAAAGAACACACAGT 461
 Qy 41 GlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaVal-LysThrTh 60
 Db 462 CAACCCACACATCACTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACAC 521
 Qy 60 rGly-----LysGlyLeuValLys-----GlyArgAsnLeuAspSerArgG1 74
 Db 522 GGGGGTCTTTTCCAGCCCTTGTCTCCCAATTGGAATTATAATATGGAAGAAGAGC 581
 Qy 74 yLeuile----- 76
 Db 582 TGTATTCTTTATCCAGCAATGTCCACTAAATTTCCCTGGGGGATTTGGGAAGATAAAA 641
 Qy 77 -----LeuGlyAlaGluAlaTrpGlyArgGlyValLys 87
 Db 642 AAGNACAAATGGGCTTGGGGCCAAACCTTGGGGCCCTTCCTCAAAA 687

RESULT 3

BI018962/c

LOCUS

DEFINITION IL3-WT0267-050101-437-A02 MT0267 Homo sapiens cDNA, mRNA sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

DIAS NETO, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

EST.

EST.

EST.

EST.


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QY      82  TipGly 83
      |||||
Db      12  TGGGGT 7

RESULT 5
AV7211179
LOCUS   AV7211179 HTB Homo sapiens cDNA clone HTBAKFl1 5', mRNA sequence.
ACCESSION
VERSION AV7211179.1 GI:10818331
KEYWORDS
SOURCE  EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
TITLE    Homo sapiens cDNA HTB clones
JOURNAL  Unpublished (2000)
COMMENT  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
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1..673
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HTBAKFl1"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="HTB"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

Alignment Scores:
Pred. No.: 1,23e-15 Length: 673
Score: 206.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.59% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x AV7211179 (1-673)

QY      22  GlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGln 41
      |||||
Db      2  GGAAGCAACATTCGAGATGGCTTCTTCTATCAAGAAATAAAGACACACAGTCAA 61

QY      42  ProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      62  CCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACAGG 121

RESULT 6
CB420818
LOCUS   CB420818
DEFINITION CB420818 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB420818
VERSION   CB420818.1 GI:29187264
KEYWORDS  EST.
SOURCE    Bos taurus (cow)
ORGANISM  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

QY      5  LeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn 24
      |||||
Db      214 CTGGTGATAACTGTGGTCCTCGAGTACCTCGGGTATTTGGAGATCCAGTTCAGGGAACAAC 273

QY      25  ThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGln 44
      |||||
Db      274 CTGTTGAAGAGTGACAGCTTTCCATCAAGAAATAAAGACACACAGAGTCAACCCACAA 333

QY      45  SerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      334 TCATCTTTAGAGATAGTGTGATACCTACCAAGGCTCTCAGCAGCACAGGA 384

RESULT 7
B1107684
LOCUS   B1107684
DEFINITION 602891529F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036647 5',
mRNA sequence.
ACCESSION B1107684
VERSION   B1107684.1 GI:14558577
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  1 (bases 1 to 855)
TITLE    NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.

Bovidae; Bovinae; Bos.
1 (bases 1 to 582)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,
Wray, J.B. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: FQY8014 row: B column: 7
Seq primer: GTAATACGACTCTACTATAGG.
Location/Qualifiers
1..582
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/clone_lib="MARC 6BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

Alignment Scores:
Pred. No.: 1,23e-11 Length: 582
Score: 174.00 Matches: 35
Percent Similarity: 77.19% Conservative: 9
Best Local Similarity: 61.40% Mismatches: 13
Query Match: 37.66% Indels: 0
DB: 14 Gaps: 0

US-09-989-293A-377 (1-90) x CB420818 (1-582)

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 504)

REFERENCE
AUTHORS
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSS: CH230-163F15-TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 163 row: F column: 15
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers
1..504
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-163F15"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/notes="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 13.5 Length: 504
Score: 79.00 Matches: 22
Percent Similarity: 46.38% Conservative: 10
Best Local Similarity: 31.88% Mismatches: 23
Query Match: 17.10% Indels: 14
DB: 28 Gaps: 1

US-09-989-293A-377 (1-90) x BH354326 (1-504)

Qy 34 ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro 53
Db 334 AGGGTTCCTGTAATTCCTTTTCACATCTCAGTCCTGAGTCTGACATATCACTATT 275

Qy 54 ThrlysalVallyThrThrGlyLysGlyLeVallyLysGlyArgAsnLeuAspSerArg 73
Db 274 TCTAAGTTAAACAAAGTCCGGTCTGTTGGTCTACTGATAGTACAGACAGAGATCTAAC 215

Qy 74 Gly-----LeulleGluGlyAla 79
Db 214 GGGAGAACTAATGCTTCCACACAGACCCCTCAGTGGAAAACTGCTTATGTGACGGCAA 155

Qy 80 GluAlaTrpGlyArgGlyVallyLys 88
Db 154 GAGGTGTTGGAGAGGGGGGGGAG 128

RESULT 14
BJ193507/c
LOCUS

DEFINITION
BJ193507 536 bp mRNA linear EST 21-OCT-2003
caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn1902 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
PubMed
COMMENT

BJ193507
BJ193507.1 GI:18361441

EST:
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 536)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)

22709184
12808149
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGGATCCAACCCCTGGAGATTTTCTTTTNN-3' was used as a 1st 3' primer, and 5'-GGTTCGATCATGCTGTTCAGACAGCGATGACTCGAGAACGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCAATCGCCGAGCTCGAATTCGCGAGAACG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).

FEATURES

Location/Qualifiers
1..536
/organism="Physcomitrella patens subsp. patens"
/mol_type="mRNA"
/sub_species="patens"
/db_xref="taxon:145481"
/clone="pphn1902"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN

Alignment Scores:
Pred. No.: 14.7 Length: 536
Score: 79.00 Matches: 28
Percent Similarity: 45.45% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 17.10% Indels: 12
DB: 12 Gaps: 4

US-09-989-293A-377 (1-90) x BJ193507 (1-536)

Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaLeuTrpArgSerAsn 20
Db 400 ATCGCTTCTCTCTTGGCTCTCTCTCTCTC-----GACCTCTTGGAGCCTCAAC 350

Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 349 AGCGGACGGCGCACCTCCAGCGGGGG-----TGCAGCGCTCATGCGGACGCCAC 296

QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
 Db 295 CCAACACCACTCCGACACTCGATCGATCGACACTCCTCTTCTCGCAAGCTT 236
 QY 61 GlyLysGlyIleValLysGlyArg-----AsnLeuAspSerArgGlyLeuIle 76
 Db 235 GCGGAA-----CAGGAGGCCAGCTATCCCTCACTGAGACATTCGGGCTTAAAC 185
 QY 77 LeuGlyAlaGluAlaTrpGlyArg 84
 Db 184 CAAAGCAGCGATCTTCTGCGCGT 161

RESULT 15

BQ406117 644 bp mRNA linear EST 22-MAY-2002
 GA_Ed0090H12f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Ed0090H12f, mRNA sequence.

ACCESSION BQ406117

VERSION

KEYWORDS BQ406117.1 GI:21093804

SOURCE

ORGANISM EST.

Gossypium arboreum

Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1. (bases 1 to 644)

Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,

Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution

of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Total High Quality bases = 584

Seq primer: TAATACGACTCACTATAGG

High quality sequence stop: 629.

Location/Qualifiers

1..644

/organism="Gossypium arboreum"

/mol_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ed0090H12f"

/tissue_type="Fibers isolated from bolls harvested 7-10

dpa"

/lab_host="E. coli"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 18.9 Length: 644

Score: 79.00 Matches: 25

Percent Similarity: 46.15% Conservative: 11

Best Local Similarity: 32.05% Mismatches: 24

Query Match: 17.10% Indels: 18

DB: 13 Gaps: 3

US-09-989-293A-377 (1-90) x BQ406117 (1-644)

QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSer-----ArgAsnLysGlu 37

Db 310 CACTCACCAACCAACAGCTGCAATGGGTTCTTTCTTCAAGACACCGTATAGCAA 369

QY 38 AsnHisSerGlnProThrGlnSerSerLeuGluAspSerVal----- 51

Db 370 CAGCAGGCACCTGCCTTCAGGATCATCAACTTCAACGTCAGTGTGTGTCATTGTTCTCCA 429
 QY 52 -----ThrProThrLysAlaValLysThrThrGlyLys 62
 Db 430 GTTACTCCTGTAACTACTGGCACCACTGACCCCTGCAAGGCTGTA---GTTGCTGCTGCT 486
 QY 63 GlyIleValLysGlyValArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
 Db 487 GGTAAATGAAAGGTGGTGGCATAGCATCACAGGACTTATACATGCTGTCACAA 540

Search completed: April 4, 2004, 09:54:24

Job time : 2717 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2004, 12:07:55 ; Search time 14 Seconds
(without alignments)
334.737 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

Sequence: 1 MFFFLSLLLLVCEAIWRN.....DSRGLLGAENGWGKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	14.8	622	TFR1_RAT	Q99376 rattus norv
2	67	14.5	226	RS5_MYCGA	O52349 mycoplasma
3	65	14.1	368	VE2_HPV52	P36796 human papil
4	64	13.9	255	RR3_CHAGL	Q8m9v0 chaetosphe
5	63.5	13.7	669	GALC_HUMAN	P54803 homo sapien
6	63.5	13.7	705	CDG5_YEAST	P32582 saccharomyc
7	63.5	13.7	882	KEL2_YEAST	P50090 saccharomyc
8	63	13.6	80	DMS6_AGAAN	Q93226 agalychnis
9	62.5	13.5	268	PYRF_PACTA	O93864 pachysolen
10	62.5	13.5	379	Y528_MUNY3	Q55518 synchocyst
11	62	13.4	1634	DPOL_METJA	Q58295 methanococc
12	61.5	13.3	401	TRM1_AERPE	Q9ydv7 aeropyrum p
13	61.5	13.3	516	MEFA_XENLA	Q03414 xenopus lae
14	61.5	13.3	834	CWFM_SCHPO	Q9p6r5 schizosacch
15	61.5	13.3	960	YMX6_YEAST	Q04279 saccharomyc
16	61	13.2	237	T4S3_HUMAN	P19075 homo sapien
17	61	13.2	415	B2AR_MACMU	Q28509 macaca mula
18	61	13.2	790	LY14_YEAST	P40971 saccharomyc
19	61	13.2	1774	MSAS_PENPA	P22367 penicillium
20	60.5	13.1	567	TGR2_RAT	P38438 rattus norv
21	60.5	13.1	676	RLM1_YEAST	Q12224 saccharomyc
22	60.5	13.1	708	ICAL_HUMAN	P20810 homo sapien
23	60.5	13.1	1369	NPAS_CHICK	O42414 gallus gall
24	60.5	13.1	1969	2292_HUMAN	O60281 homo sapien
25	60.5	13.1	2298	CU05_HUMAN	Q9y3r5 homo sapien
26	60	13.0	653	RAE1_HUMAN	P24386 homo sapien
27	60	13.0	671	NCPR_MUSDO	Q07994 musca domes
28	60	13.0	938	SVI_BUCBP	Q8k922 buchnera ap
29	60	13.0	939	SVI_BUCBP	Q89au9 buchnera ap
30	60	13.0	962	SUUR_DROME	Q9vt82 drosophila
31	60	13.0	1503	KRP6_HUMAN	Q95255 homo sapien
32	59.5	12.9	576	UN87_CABEL	P37806 caenorhabdi
33	59	12.8	202	RUVA_PSESM	Q87y34 pseudomonas

RESULT 1

ID	TFR1_RAT	STANDARD;	PRT;	622 AA.
AC	Q99376;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Transferrin receptor protein 1 (Tfr1) (Tfr) (TFR) (Tfrf) (Fragment).			
GN	TFR1 OR TFRF.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=9125359; PubMed=2126342;			
RA	Roberts K.P., Griswold M.D.;			
RT	"Characterization of rat transferrin receptor cDNA: the regulation of			
RT	transferrin receptor mRNA in testes and in Sertoli cells in culture."			
RL	Mol. Endocrinol. 4:531-542(1990).			
CC	-I- FUNCTION: Cellular uptake of iron occurs via receptor-mediated			
CC	endocytosis of ligand-occupied transferrin receptor into			
CC	specialized endosomes. Endosomal acidification leads to iron			
CC	release. The apotransferrin-receptor complex is then recycled to			
CC	the cell surface with a return to neutral pH and the concomitant			
CC	loss of affinity of apotransferrin for its receptor. Transferrin			
CC	receptor is necessary for development of erythrocytes and the			
CC	nervous system (By similarity).			
CC	-I- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin			
CC	molecule per polypeptide chain (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).			
CC	-I- TISSUE SPECIFICITY: In testis, expressed in Sertoli cells,			
CC	peritubular myoid cells and in germinal cells. Highest levels in			
CC	Sertoli cells.			
CC	-I- PTM: N- and O-glycosylated, phosphorylated and palmitoylated (By			
CC	similarity).			
CC	-I- SIMILARITY: Belongs to peptidase family M28B.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; M58040; AAA42273.1; --			
DR	PIR; A34549; A34549.			
DR	HSSP; P02786; 1CX8.			
DR	InterPro; IPR003137; PA.			
DR	InterPro; IPR007484; Peptidase_M28.			
DR	InterPro; IPR007365; TFR_dimer.			
DR	Pfam; PF02225; PA; 1.			
DR	Pfam; PF04389; Peptidase_M28; 1.			
DR	Pfam; PF04253; TFR_dimer; 1.			

ALIGNMENTS

34	59	12.8	641	1	UGS2_SOLTU
35	59	12.8	708	1	MM09_RAT
36	59	12.8	719	1	CLID_BACTU
37	59	12.8	793	1	YF06_MYCPN
38	59	12.8	970	1	DAB1_YEAST
39	59	12.8	1116	1	MRH1_SCHPO
40	58.5	12.7	417	1	OXLT_OXAFO
41	58.5	12.7	439	1	QUIX_ACICA
42	58.5	12.7	531	1	SIS2_CANTR
43	58.5	12.7	542	1	THS_METJA
44	58.5	12.7	953	1	LKA1_PASHA
45	58.5	12.7	953	1	LKA3_PASHA

P93568	solanum tub
P50282	rattus norv
Q9xdl1	bacillus th
P75280	mycoplasma
P21657	saccharomyc
Q10407	schizosacch
Q51330	oxalobacter
Q43923	actinobacter
Q12600	candida tro
Q58405	methanococc
P16535	pasteurella
P55116	pasteurella


```
CC -----
DR EMBL; X74481; CAAS2588.1; -.
DR PIR; S36576; S36576.
DR HSP; P17383; 1DHM.
DR InterPro; IPR000427; E2.C.
DR InterPro; IPR001866; E2.N.
DR InterPro; IPR009021; Viral_DNA_bd.
DR Pfam; PF00511; E2.C; 1.
DR Pfam; PF00508; E2.N; 1.
DR ProDom; PD000672; E2.C; 1.
DR ProDom; PD000678; E2.N; 1.
KW Early protein; Transcription regulation; Activator; DNA-binding;
Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 368 AA; 4739 MW; 3212B423B2F629D3 CRC64;

Query Match 14.1%; Score 65; DB 1; Length 368;
Best Local Similarity 27.0%; Pred. No. 15;
Matches 24; Conservative 11; Mismatches 40; Indels 14; Gaps 3;

QY 10 LIVCEAIWNSGNSNTLENGYFLSRN-----KENHSOPTQSSLEDSVTPTKAVK 58
DB 192 VIVCPASVSNSVEVSTT-ETAVHLCTETSKTSVSVGAKDHLQPPOKRRRPDVTDSRNTK 250
QY 59 TTCKGIVKGNLDS--RGLILGAEAWGRG 85
DB 251 YFNNILRGQSVDSVTRGLVTATECTNKG 279

RESULT 4
RR3_CHAGL STANDARD; PRT; 255 AA.
AC QM3YVO;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Chaetosphaeridium globosum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Coleochaetales;
OC Chaetosphaeridiaceae; Chaetosphaeridium.
OC NCBI_TaxID=96477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1311;
RX MEDLINE=22177139; PubMed=12161560;
RA Turmel M., Otis C., Lemieux C.;
RT "The chloroplast and mitochondrial genome sequences of the charophyte
RT Chaetosphaeridium globosum: insights into the timing of the events
RT that restructured organelle DNAs within the green algal lineage that
RT led to land plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:11275-11280(2002).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the S3p family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF94278; AAM96576.1; -.
CC HAMAP; MF_01309; -.
CC InterPro; IPR009019; KH prok.
CC InterPro; IPR004044; KH_TYPE_2.
CC InterPro; IPR001351; Ribosomal_S3_C.
CC InterPro; IPR008282; Ribosomal_S3_N.
CC InterPro; IPR005704; S3 bact.
CC Pfam; PF00189; Ribosomal_S3_C; 1.

Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRFAMs; TIGR01009; rpsC_bact; 1.
PROSITE; PS00823; KH_TYPE_2; FALSE_NEG.
DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
FT DOMAIN 51 124 KH TYPE-2.
SQ SEQUENCE 255 AA; 29494 MW; 0A88CEB18062EAC1 CRC64;

Query Match 13.9%; Score 64; DB 1; Length 255;
Best Local Similarity 30.3%; Pred. No. 13;
Matches 27; Conservative 9; Mismatches 35; Indels 18; Gaps 4;

QY 14 EAIWNSGNSNTLENGYF---LSRNKENSQPT-----QSSLEDSVTPTKAVTKG-- 62
DB 127 EKWRYVQESLTLNSGKFRMTLSKYSNPYKEANIVAEYIARQLNENRVAFFRAMKQAIKDA 186
QY 63 ----GIVKGNLDSRGLILGAE-----AWGR 84
DB 187 KENGQVKGIKIQISGRILNGAETARVEWAR 215

RESULT 5
GALC_HUMAN STANDARD; PRT; 669 AA.
AC P54803;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Galactocerebrosidase precursor (EC 3.2.1.46) (GALCERase)
DE (Galactosylceramide) (Galactosylceramide beta-galactosidase)
DE (Galactocerebroside beta-galactosidase).
GN GALC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RC TISSUE=Placenta, and Skin fibroblast;
RX MEDLINE=94128088; PubMed=8297359;
RA Sakai N., Inui K., Fujii N., Fukushima H., Nishimoto J.,
RA Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
RT "Krabbe disease: isolation and characterization of a full-length cDNA
RT for human galactocerebrosidase.";
RL Biochem. Biophys. Res. Commun. 198:485-491(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 27-59 AND 436-454.
RC TISSUE=Brain, and Testis;
RX MEDLINE=94108435; PubMed=8281145;
RA Chen Y.Q., Rafi M.A., de Gala G., Wenger D.A.;
RA "Cloning and expression of cDNA encoding human galactocerebrosidase,
RA the enzyme deficient in globoid cell leukodystrophy.";
RL Hum. Mol. Genet. 2:1841-1845(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT THR-546.
RX MEDLINE=95324938; PubMed=7601472;
RA Luzzi P., Rafi M.A., Wenger D.A.;
RA "Structure and organization of the human galactocerebrosidase (GALC)
RA gene.";
RL Genomics 26:407-409(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98094242; PubMed=9434153;
RA Sakai N., Fukushima H., Inui K., Fu L., Nishigaki T., Yanagihara I.,
RA Tatsumi N., Ozono K., Okada S.;
RA "Human galactocerebrosidase gene: promoter analysis of the 5'-flanking
RA region and structural organization.";
RL Biochim. Biophys. Acta 1395:62-67(1998).
RN [5]
RP SEQUENCE OF 27-45 AND 436-454, AND CHARACTERIZATION.
RX TISSUE=Urine;
RX MEDLINE=94002192; PubMed=8399327;
RA Chen Y.Q., Wenger D.A.;
```

RT "Galactocerebrosidase from human urine: purification and partial
RT characterization.";
RN Biochim. Biophys. Acta 1170:53-61(1993).
RN [6]
RN REVIEW ON GLD MUTATIONS.
RX MEDLINE=97478285; PubMed=9338580;
RA Wenger D.A., Rafi M.A., Luzzi P.;
RT "Molecular genetics of Krabbe disease (globoid cell leukodystrophy):
RT diagnostic and clinical implications.";
RL Hum. Mutat. 10:268-279(1997).
RN [7]
RN REVIEW ON VARIANTS.
RX MEDLINE=20295342; PubMed=10833326;
RA Wenger D.A., Rafi M.A., Luzzi P., Datto J., Costantino-Ceccarini E.;
RT "Krabbe disease: Genetic aspects and progress toward therapy.";
RL Mol. Genet. Metab. 70:1-9(2000).
RN [8]
RN VARIANT CYS-168.
RX MEDLINE=96090246; PubMed=7581365;
RA Rafi M.A., Luzzi P., Chen Y.Q., Wenger D.A.;
RT "A large deletion together with a point mutation in the GALC gene is a
RT common mutant allele in patients with infantile Krabbe disease.";
RL Hum. Mol. Genet. 4:1285-1289(1995).
RN [9]
RN VARIANTS GLD ALA-302 AND GLY-550.
RX MEDLINE=96121583; PubMed=8595408;
RA Tatsumi N., Inui K., Sakai N., Fukushima H., Nishimoto J.,
RA Yanagihara I., Nishigaki T., Tsukamoto H., Fu L., Tanikie M.,
RA Okada S.;
RT "Molecular defects in Krabbe disease.";
RL Hum. Mol. Genet. 4:1865-1868(1995).
RN [10]
RN VARIANTS GLD HIS-63; SER-95; LEU-101; THR-234; SER-268 AND CYS-298,
RN AND VARIANT THR-546.
RX MEDLINE=97094180; PubMed=8940268;
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,
RA MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.;
RT "Molecular heterogeneity of late-onset forms of globoid-cell
RT leukodystrophy.";
RL Am. J. Hum. Genet. 59:1233-1242(1996).
RN [11]
RN ERRATUM.
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,
RA MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.;
RL Am. J. Hum. Genet. 60:1264-1264(1997).
RN [12]
RN VARIANTS GLD ASN-528 AND SER-583.
RX MEDLINE=96198195; PubMed=8786069;
RA Rafi M.A., Luzzi P., Zlotogora J., Wenger D.A.;
RT "Two different mutations are responsible for Krabbe disease in the
RT Druze and Moslem Arab populations in Israel.";
RL Hum. Genet. 97:304-308(1996).
RN [13]
RN VARIANTS GLD MET-66; ASP-270 AND SER-618, AND VARIANTS VAL-289 AND
RN THR-546.
RX MEDLINE=97418134; PubMed=9272171;
RA Fukuya H., Kukita Y.-J., Nagano S., Sakai Y., Yamashita Y.,
RA Furuya K., Inatomi Y., Saito Y., Koike R., Tsuji S., Fukumaki Y.,
RA Hayashi K., Kobayashi T.;
RT "Adult onset globoid cell leukodystrophy (Krabbe disease): analysis of
RT galactosylceramidase cDNA from four Japanese patients.";
RL Hum. Genet. 100:450-456(1997).
RN [14]
RN VARIANTS GLD ASP-270 AND ARG-537, AND VARIANT THR-625.
RX MEDLINE=99406501; PubMed=10477434;
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,
RA Raghavan S., Kolodny E.H.;
RT "Molecular basis of late-life globoid cell leukodystrophy.";
RL Hum. Mutat. 14:256-262(1999).
RN [15]
RN VARIANTS GLD ARG-43; PHE-52; ILE-262; CYS-319; GLY-410; HIS-515 AND
RN ARG-652.
RX MEDLINE=99250870; PubMed=10234611;

RA Fu L., Inui K., Nishigaki T., Tateumi N., Tsukamoto H., Kokubu C.,
RA Muramatsu T., Okada S.;
RT "Molecular heterogeneity of Krabbe disease.";
RL J. Inher. Metab. Dis. 22:155-162(1999).
RN [16]
RN FUNCTION: Hydrolyzes the galactose ester bonds of
CC galactosylceramide, galactosylsphingosine, lactosylceramide, and
CC monogalactosylglyceride. Enzyme with very low activity
CC responsible for the lysosomal catabolism of galactosylceramide, a
CC major lipid in myelin, kidney and epithelial cells of small
CC intestine and colon.
CC CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)O = D-
CC galactose + N-acylsphingosine.
CC SUBCELLULAR LOCATION: Lysosomal.
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P54803-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P54803-2; Sequence=VSP_001800, VSP_001801;
CC TISSUE SPECIFICITY: Highest level of activity in testes compared
CC to brain, kidney, placenta and liver. Can also be found in urine.
CC POLYMORPHISM: Polymorphic amino-acid changes are responsible for
CC the wide range of catalytic activities found in the general
CC population.
CC DISEASE: Defects in GALC are the cause of globoid cell
CC leukodystrophy (GLD) [MIM:245200]; also known as Krabbe disease.
CC This autosomal recessive disorder results in the insufficient
CC catabolism of several galactolipids that are important in the
CC production of normal myelin. Clinically, the most frequent form is
CC the infantile form. Most patients (90%) present before six months
CC of age with irritability, spasticity, arrest of motor and mental
CC development, and bouts of temperature elevation without infection.
CC This is followed by myoclonic jerks of arms and legs,
CC opisthotonus, hypertonic fits, and mental regression, which
CC progresses to a severe decerebrate condition with no voluntary
CC movements and death from respiratory infections or cerebral
CC hyperpyrexia before 2 years of age. However, a significant number
CC of cases with later onset, presenting with unexplained blindness,
CC weakness and/or progressive motor, and sensory neuropathy that can
CC progress to severe mental incapacity and death, have been
CC identified.
CC MISCELLANEOUS: Has an optimal pH between 4.0 and 4.4. Activity is
CC lost when heated at 52 degrees Celsius for five minutes.
CC SIMILARITY: Belongs to family 59 of glycosyl hydrolases.
CC DATABASE: NAME=GeneDis; NOTE=Krabbe disease;
CC WWW=http://life2.tau.ac.il/GeneDis/Tables/Krabbe/Krabbe.html".

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CC EMBL; D25283; BAA04971.1; -
CC EMBL; D25284; BAA04972.1; -
CC EMBL; L23116; AAA16645.1; -
CC EMBL; L38559; AAA80975.1; -
CC EMBL; L38544; AAA80975.1; JOINED.
CC EMBL; L38545; AAA80975.1; JOINED.
CC EMBL; L38546; AAA80975.1; JOINED.
CC EMBL; L38547; AAA80975.1; JOINED.
CC EMBL; L38548; AAA80975.1; JOINED.
CC EMBL; L38549; AAA80975.1; JOINED.
CC EMBL; L38550; AAA80975.1; JOINED.
CC EMBL; L38551; AAA80975.1; JOINED.
CC EMBL; L38552; AAA80975.1; JOINED.
CC EMBL; L38553; AAA80975.1; JOINED.
CC EMBL; L38555; AAA80975.1; JOINED.
CC EMBL; L38556; AAA80975.1; JOINED.
CC EMBL; L38557; AAA80975.1; JOINED.
CC EMBL; L38558; AAA80975.1; JOINED.

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DR EMBL; D86181; BAA24902.1; -.
DR EMBL; D84232; BAA24902.1; JOINED.
DR EMBL; D84233; BAA24902.1; JOINED.
DR EMBL; D84234; BAA24902.1; JOINED.

Query Match      13.7%; Score 63.5; DB 1; Length 669;
Best Local Similarity 23.5%; Pred. No. 43;
Matches 20; Conservative 15; Mismatches 43; Indels 7; Gaps 1;

QY 5 LSLILLVCEATWRSNGTLENGYFLSRNKENHSQPTQSSLEDSTVTKAVKTTGKGI 64
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 LQVKIIASDNLMESIASMLLDALFKVVDVIGAHYPGTHSAKDA-----KLTGKKL 254
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 65 VKGNLDSRLGLIGABAGRGVKN 89
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 255 WSEDFSTLNSDMGACGWRLNQ 279
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
ID CDC5_YEAST STANDARD; PRT; 705 AA.
AC P32562;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37).
GN CDC5 OR PKX2 OR MSP2 OR YMR001C OR YMR270.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RC STRAIN=A364A;
RP SEQUENCE FROM N.A.
RX MEDLINE=93309479; PubMed=8321244;
RA Kitada K., Sugino A., Johnson L.H., Johnson A.L.;
RA "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
RT cycle mutant gene dbf4 encodes a protein kinase and is identified as
RT CDC5";
RL Mol. Cell. Biol. 13:4445-4457(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churche C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moulé S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrrell B.G.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
RN [3]
RP PHOSPHORYLATION OF SCCL.
RX MEDLINE=21264235; PubMed=11371343;
RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.-A., Nasmyth K.;
RA "Phosphorylation of the cohesin subunit Sccl by Polo/Cdc5 Kinase
RT regulates sister chromatid separation in yeast.";
RL Cell 105:459-472(2001)
CC -!- FUNCTION: Protein kinase required for the cell cycle.
CC Phosphorylates SCCL/MCD1.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC CDC5/Polo subfamily.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC -----
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DR EMBL; M84220; AAA02576.1; -.
DR EMBL; Z48613; CA888516.1; -.
DR EIR; A48144; A48144.
DR HSP; Q63450; IA06.
DR Germonline; 142669; -.
DR SGD; S0004603; CDC5.
DR GO; GO:0005935; C:bud neck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0000922; C:spindle pole; IDA.
DR GO; GO:0006263; P:DNA dependent DNA replication; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr pkin AS.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00669; pkinase; 1.
DR Pfam; PF00659; POLO box; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50078; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Cell division; Serine/threonine-protein kinase;
KW Transferase; ATP-binding; Repeat.
FT DOMAIN 82 337 PROTEIN KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT_SITE 204 204 BY SIMILARITY.
FT DOMAIN 520 587 POLO BOX 1.
FT DOMAIN 619 692 POLO BOX 2.
FT SEQUENCE 705 AA; 81030 MW; B5A25F1BBBAA3DC CRC64;
SQ
Query Match      13.7%; Score 63.5; DB 1; Length 705;
Best Local Similarity 31.2%; Pred. No. 46;
Matches 15; Conservative 6; Mismatches 22; Indels 5; Gaps 1;

QY 32 LSRNKENHSQPTQSSLEDSTV-----TPTKAVKTTGKGI VKGRNLDSSG 74
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 45 LDPNDHHHQPQAQKKREKLSALCKTPPSLIKTRGDKYHRRHFLGEGG 92
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
KE2_YEAST STANDARD; PRT; 882 AA.
ID KE2_YEAST
AC P50090;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kelch repeats protein 2
GN KE2 OR YGR238C OR G8585.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96267763; PubMed=8701610;
RA van der Aart Q.J.M., Kleine K., Steensma H.Y.;
RA "Sequence analysis of the 43 kb CRM1-YLM9-pET54-DIE2-SM11-PHO81-YHB4-
RT PKI region from the right arm of Saccharomyces cerevisiae chromosome
RT VII.";
RL Yeast 12:385-390(1996).
RN [2]
RN CHARACTERIZATION.
RP MEDLINE=99003296; PubMed=9786949;
RX Phillips J., Herskowitz I.;
RA "Identification of Kelp1, a kelch domain-containing protein involved
RT in cell fusion and morphology in Saccharomycetes cerevisiae.";
RL J. Cell Biol. 143:375-389(1998).
RL
```

CC -!- SUBUNIT: Interacts with KELL.
CC -!- SIMILARITY: Contains 4 Kelch repeats.
CC -!- SIMILARITY: TO YEAST KELL AND S.POMBE SPAC6G10.02C.
CC
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CC
CC EMBL; X87941; CAA61189.1; -
CC EMBL; 273023; CAA97266.1; -
CC PIR; S57704; S57704.
CC GeneOnline; 141550; -
CC SGD; S0003470; KEL2.
CC GO; GO:0005935; C:bud neck; IDA.
CC GO; GO:0005934; C:bud tip; IDA.
CC GO; GO:0005937; C:shmoo tip; IDA.
CC GO; GO:0000747; P:conjugation with cellular fusion; IGI.
CC InterPro; IPR006652; Kelch_rep.
CC Pfam; PF01344; Kelch; 4.
CC KW Kelch repeat; Repeat; Coiled coil.
CC FT REPEAT 99 143
CC FT REPEAT 213 267
CC FT REPEAT 268 317
CC FT REPEAT 319 369
CC FT REPEAT 550 685
CC FT DOMAIN 728 881
CC FT COILED COIL (POTENTIAL).
CC FT COILED COIL (POTENTIAL).
CC SQ SEQUENCE 882 AA; 99974 MW; 63B9772FF017E6D9 CRC64;
Query Match 13.7%; Score 63.5; DB 1; Length 882;
Best Local Similarity 20.8%; Pred. No. 59;
Matches 26; Conservative 20; Mismatches 34; Indels 45; Gaps 4;
QY 11 LVCEAIWRNSGNTLENGYFLSRNKHNSQPT-----Q 44
DB 418 IMCESLHAGESFNSLSGGTSPKSTESNQEIINILTPRDPKSVLSYNDIDEGAGSYS 477
QY 45 SLEDSVTPTKA-----VKTTGKGI-VKGRNLD-SRGLILGAEAWGRG 85
DB 478 SALDDKAFERKSDREERKPKSQSVDSINKESPTGKIVKKNFVPLVRLGLTVDSERYGSS 537
QY 86 VKKNT 90
DB 538 SYKDT 542
RESULT 8
DMS6 AGAAN
ID DMS6 AGAAN STANDARD; PRT; 80 AA.
AC O93226;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dermaseptin AA-3-6 precursor.
OS Agalychnis anae (Yellow-eye leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Phyllomedusinae; Agalychnis.
OX NCBI_TaxID=75990;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE-Skin;
RX MEDLINE=98449786; PubMed=9774745;
RA Wechsberger C.;
RL "Cloning of cDNAs encoding new peptides of the dermaseptin-family.";
RL Biochim. Biophys. Acta 1388:279-283(1998).
CC -!- FUNCTION: Possesses a potent antimicrobial activity against Gram-
CC positive and Gram-negative bacteria. Probably acts by disturbing
CC membrane functions with its amphipathic structure (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
CC
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CC
CC EMBL; AJ005188; CAA06425.1; -
CC InterPro; IPR004275; Brevenin.
CC Pfam; PF03032; Brevenin; 1.
CC KW Amphibian defense peptide; Antibiotic; Multigene family;
CC KW Cleavage on pair of basic residues; Amidation; Signal.
CC SIGNAL 1 22
CC FT PROPEP 23 43
CC FT PEPTIDE 46 77
CC FT PROPEP 79 80
CC FT MOD_RES 77 77
CC FT AMIDATION (G-78 PROVIDE AMIDE GROUP)
CC FT (POTENTIAL)
CC FT SEQUENCE 80 AA; 8817 MW; DB13FD831E7E2140 CRC64;
Query Match 13.6%; Score 63; DB 1; Length 80;
Best Local Similarity 27.1%; Pred. No. 4.5;
Matches 23; Conservative 12; Mismatches 32; Indels 18; Gaps 4;
QY 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRNKHNSQPTQSLSDSVTPTKAVKIT 60
DB 10 LVLFGLVLSLSCIEEEKEN-----EDEEEQEDQSEMKKGMWST--IRNV 54
QY 61 GKGIVKGRNLDGRGLILGA--EAWG 83
DB 55 GKSRAKAANLPKA-ALGALSEAVG 78
RESULT 9
PYRF PACTA STANDARD; PRT; 268 AA.
ID PYRF PACTA STANDARD; PRT; 268 AA.
AC O93864;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
DE (OMPDCase) (OMPDecase) (Uridine 5'-monophosphate synthase) (UMP
DE synthase).
GN URA3.
OS Pachysolen tannophilus (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pachysolen.
OX NCBI_TaxID=4918;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark-Walker G.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
CC -!- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
CC -!- SIMILARITY: Belongs to the OMP decarboxylase family.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF047170; AAD02431.1; -
CC HSP; P03962; IDOW.
CC InterPro; IPR001754; OMPDecase.
CC Pfam; PF00215; OMPDecase; 1.
DR

```
DR PROSITE: PS00156; OMEDECASE; 1.
KW Pyrimidine biosynthesis; Lyase; Decarboxylase.
FT ACT SITE 95 BY SIMILARITY.
SQ SEQUENCE 268 AA; 29684 MW; ECC89602DA2FC10A CRC64;

Query Match 13.5%; Score 62.5; DB 1; Length 268;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 21; Conservative 8; Mismatches 23; Indels 21; Gaps 2;

QY 20 NSGNTLNGYFLSRNKHNSPTQSSLEDSVTPKAVKTTGKIVKG-----RNLD 72
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 101 NTVKQYKNGIF-----KIAQWADIINAHGVTGEGIVKGLKEAALETTL 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 73 RGLILCAEAWGRG 85
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 147 RGLILAEILSSKG 159

RESULT 10
Y528 SNNY3
ID Y528_SNNY3 STANDARD; PRT; 379 AA.
AC Q55518;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sl10528 (EC 3.4.24.-).
GN SL10528.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to peptidase family M50B.
CC -1- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D64006; BAA10876.1; -.
CC PIR; S76029; S76029.
CC MEROPS; M50.UPB; -.
CC InterPro; IPR000644; CBS domain.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR008915; Peptidase_M50.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF02163; Peptidase_M50; 1.
CC SMART; SM00116; CBS; 2.
CC DR DR
CC KW Hypothetical protein; Hydrolase; 1.
CC Repeat; CBS domain; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT DOMAIN 260 310 CBS 1.
FT DOMAIN 327 375 CBS 2.
FT METAL 75 75 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 76 76 BY SIMILARITY.
```

```
FT METAL 79 79 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 379 AA; 40465 MW; 1CC3251660078ECB CRC64;

Query Match 13.5%; Score 62.5; DB 1; Length 379;
Best Local Similarity 26.5%; Pred. No. 29;
Matches 22; Conservative 13; Mismatches 41; Indels 7; Gaps 1;

QY 5 LSLILLVCEAIWRSNNGSNTLENGYFLSRNKHNSPTQSSLEDSVTPKAVKTTGKI 64
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 211 LGLILNLPISFWTILIGFWLLQAGSSARNAQVKEQMEAFDAEDAVIPNSPII 270
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 65 -----VKGRNLDSDRGLILGAE 80
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 271 REFANDYVIGTKPMRRFLVIGAD 293

RESULT 11
DPOL METJA
ID DPOL_METJA STANDARD; PRT; 1634 AA.
AC Q58295;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
DE intein].
DE POL OR MJ0885.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RT Science 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N).
CC -1- PTM: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the intervening region (intein)
CC followed by peptide ligation (Potential).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67532; AAB98889.1; -.
CC HSP; P56689; ITG0.
CC TIGR; MJ0885; -.
CC InterPro; IPR006172; DNA_pol_B.
CC InterPro; IPR006134; DNA_pol_B_dom.
CC InterPro; IPR006133; DNA_pol_B-exo.
CC InterPro; IPR003587; Hedgehog_hint_N.
CC InterPro; IPR003586; Hedgehog_hint_C.
CC InterPro; IPR006142; INTEIN.
CC InterPro; IPR004042; Intein_endonuc.
CC InterPro; IPR006141; Intein_S.
CC InterPro; IPR004578; Pol2.
CC Pfam; PF00136; DNA_pol_B; 3.
```

PFam: PF003104; DNA pol B exo; 1.
 PRINTS; PR00379; INTEIN.
 SMART; SM00305; Hintc; 2.
 SMART; SM00306; Hintc; 2.
 SMART; SM00486; POLBc; 1.
 TIGRFAMs; TIGR01443; inEIN_Cterm; 2.
 TIGRFAMs; TIGR01445; inEIN_Nterm; 2.
 TIGRFAMs; TIGR00592; POL2; 1.
 PROSITE; PS00116; DNA POLYMERASE B; 1.
 PROSITE; PS00818; INTEIN_C_TER; 2.
 PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
 PROSITE; PS00817; INTEIN_N_TER; 2.
 TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
 DNA-binding; Autocatalytic cleavage; Protein splicing;
 Complete proteome.
 CHAIN 1 425 POL, 1ST PART (POTENTIAL).
 CHAIN 426 794 MJA POL-1 INTEIN (POTENTIAL).
 CHAIN 795 882 POL, 2ND PART (POTENTIAL).
 CHAIN 883 1358 MJA POL-2 INTEIN (POTENTIAL).
 CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
 SEQUENCE 1634 AA; 191708 MW; 84A1FAFAB1F97DDO CRC64;
 Query Match 13.4%; Score 62; DB 1; Length 1634;
 Best Local Similarity 29.2%; Pred. No. 1.7e+02;
 Matches 21; Conservative 9; Mismatches 24; Indels 18; Gaps 4;
 QY 25 TLENGYFLSRKKNHSGPTQSSLEDSVT-----PTKAVKTTGKGVKGRNLSRGLI 76
 Db 402 TYEGGV-----KEPEKMFEDIIISDFRCHPKTKV-VKGVINIEDVKEGVY 452
 QY 77 LGAEAWGRGVKK 88
 Db 453 LGIDGWCK-VKX 463
 RESULT 12
 TRM1_AERPE STANDARD; PRT; 401 AA.
 ID MEFA_XENLA
 AC Q9YD7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32)
 DE (tRNA(guanine-26,N(2)-N(2)) methyltransferase)
 DE dimethylguanosine-26 methyltransferase
 DE (tRNA(m(2,G26)dimethyltransferase).
 GN TRM1 OR AFE0782.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 CC -!- FUNCTION: Dimethylates a single guanine residue at position 26 of
 CC a number of tRNAs using S-adenosyl-L-methionine as donor of the
 CC methyl groups (By similarity).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
 CC homocysteine + tRNA containing N(2)-methylguanine.
 CC -!- SIMILARITY: Belongs to the TRM1 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC EMBL; AP000060; BAA79760.1; ALT_INIT.
 DR HAMAP; MF_00290; -; 1.
 DR InterPro; IPR002905; TRM.
 DR Pfam; PF02005; TRM; 1.
 DR TIGRFAMs; TIGR00308; TRM1; 1.
 DR Transferase; Methyltransferase; tRNA processing; Complete proteome.
 SQ SEQUENCE 401 AA; 43034 MW; 570005B39B83366E CRC64;
 Query Match 13.3%; Score 61.5; DB 1; Length 401;
 Best Local Similarity 29.9%; Pred. No. 40;
 Matches 23; Conservative 12; Mismatches 27; Indels 15; Gaps 3;
 QY 20 NGSNTLENGYFLSRKKNHSGPTQSSLEDSVT-----TKAVKTTGKGI 64
 Db 105 NARANGLEFGSYMFNKSNSLMFHLRSRPTFVSLIDIDPYGSPAPFVDAALALSGKT 164
 QY 65 VKGRNLSRGLILGAE 81
 Db 165 VVAMTATDLAVLEGKA 181
 RESULT 13
 MEFA_XENLA STANDARD; PRT; 516 AA.
 ID MEFA_XENLA
 AC Q03414;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myocyte-specific enhancer factor 2A homolog (serum response factor-
 DE like protein 2) (SL-2).
 GN MEF2A OR SL2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neurula;
 RX MEDLINE=9309873; PubMed=1281451;
 RA Chambers A.E., Kotecha S., Towers N., Mohun T.J.;
 RA "Muscle-specific expression of SRF-related genes in the early embryo
 of Xenopus laevis.";
 RT EMBO J. 11:4981-4991(1992).
 RL -!- FUNCTION: MAY REGULATE MUSCLE-SPECIFIC TRANSCRIPTION IN THE
 CC EMBRYO AND MAY REGULATE TRANSCRIPTION OF A VARIETY OF CELL TYPES
 CC IN THE ADULT. IT BINDS TO THE SEQUENCE CTA(T/A)ATAT.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: RESTRICTED TO THE SOMITIC MESODERM OF EARLY
 CC EMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE TADPOLE.
 CC EXPRESSED IN ALL TISSUES EXAMINED IN THE ADULT.
 CC -!- DEVELOPMENTAL STAGE: Expression begins in the early neurula.
 CC -!- SIMILARITY: Belongs to the MEF2 family.
 CC -!- SIMILARITY: Contains 1 MADS-box domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; Z19123; CAA79530.1; -.
 DR PIR; S28060; S28060.
 DR HSP; P11831; 1SR5.
 DR TRANSFAC; T01784; -.

PFam: PF003104; DNA pol B exo; 1.
 PRINTS; PR00379; INTEIN.
 SMART; SM00305; Hintc; 2.
 SMART; SM00306; Hintc; 2.
 SMART; SM00486; POLBc; 1.
 TIGRFAMs; TIGR01443; inEIN_Cterm; 2.
 TIGRFAMs; TIGR01445; inEIN_Nterm; 2.
 TIGRFAMs; TIGR00592; POL2; 1.
 PROSITE; PS00116; DNA POLYMERASE B; 1.
 PROSITE; PS00818; INTEIN_C_TER; 2.
 PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
 PROSITE; PS00817; INTEIN_N_TER; 2.
 TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
 DNA-binding; Autocatalytic cleavage; Protein splicing;
 Complete proteome.
 CHAIN 1 425 POL, 1ST PART (POTENTIAL).
 CHAIN 426 794 MJA POL-1 INTEIN (POTENTIAL).
 CHAIN 795 882 POL, 2ND PART (POTENTIAL).
 CHAIN 883 1358 MJA POL-2 INTEIN (POTENTIAL).
 CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
 SEQUENCE 1634 AA; 191708 MW; 84A1FAFAB1F97DDO CRC64;
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 Db 402 TYEGGV-----KEPEKMFEDIIISDFRCHPKTKV-VKGVINIEDVKEGVY 452
 QY 77 LGAEAWGRGVKK 88
 Db 453 LGIDGWCK-VKX 463
 RESULT 12
 TRM1_AERPE STANDARD; PRT; 401 AA.
 ID MEFA_XENLA
 AC Q9YD7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32)
 DE (tRNA(guanine-26,N(2)-N(2)) methyltransferase)
 DE dimethylguanosine-26 methyltransferase
 DE (tRNA(m(2,G26)dimethyltransferase).
 GN TRM1 OR AFE0782.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 CC -!- FUNCTION: Dimethylates a single guanine residue at position 26 of
 CC a number of tRNAs using S-adenosyl-L-methionine as donor of the
 CC methyl groups (By similarity).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
 CC homocysteine + tRNA containing N(2)-methylguanine.
 CC -!- SIMILARITY: Belongs to the TRM1 family.
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Search completed: March 31, 2004, 12:14:02
Job time : 15 secs

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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:11:36 ; Search time 20 Seconds
(without alignments)
432.862 Million cell updates/sec

Title: US-09-989-293a-377
Perfect score: 462
Sequence: 1 MTFFLSLLLLVCEAIWRNS.....DSRGLILGAEWGRGVKKNT 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: Pirl:
2: Pirl:
3: Pirl:
4: Pirl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	15.2	256	AE1734	anti-repressor hom
2	68.5	14.8	495	S76967	hypothetical prote
3	68.5	14.8	622	A34549	transferrin rece
4	68	14.7	280	E82099	phosphatidate cyti
5	68	14.7	1334	T41524	rho1 gdp-gtp excha
6	66.5	14.4	337	A83026	hypothetical prote
7	66.5	14.4	479	S41015	transcription fact
8	66	14.3	851	T47495	hypothetical prote
9	65	14.1	313	A82436	transcription regu
10	65	14.1	360	H97313	protein distantly
11	65	14.1	368	S36576	E2 protein - human
12	65	14.1	379	T24554	hypothetical prote
13	64.5	14.0	532	T06029	hypothetical prote
14	64	13.9	257	A11442	anti-repressor (Ba
15	64	13.9	430	T46099	hypothetical prote
16	64	13.9	548	T28910	hypothetical prote
17	63.5	13.7	598	A64594	site-specific DNA-
18	63.5	13.7	651	A96781	unknown protein F9
19	63.5	13.7	769	I54205	galactosylceramida
20	63.5	13.7	705	A48144	protein kinase CDC
21	63.5	13.7	850	T14472	S-receptor kinase
22	63.5	13.7	882	S57704	hypothetical prote
23	63	13.6	249	T00169	anti repressor - S
24	63	13.6	250	H89989	anti repressor (im
25	63	13.6	441	H86185	hypothetical prote
26	63	13.6	457	E96572	protein FlzW16.8 [
27	63	13.6	2425	D69426	surface layer prote
28	62.5	13.5	379	S76029	hypothetical prote
29	62.5	13.5	381	T19402	hypothetical prote

30	62.5	13.5	617	2	AF2897	conserved hypothet
31	62.5	13.5	641	2	H97672	hypothetical prote
32	62.5	13.5	849	1	S51527	S-receptor kinase
33	62.5	13.5	1123	2	AD2045	hypothetical prote
34	62.5	13.5	1553	2	T18502	hypothetical prote
35	62	13.4	84	2	F81128	probable lipoprote
36	62	13.4	149	2	S76835	hypothetical prote
37	62	13.4	613	2	A88448	protein C45G9.6 [i
38	62	13.4	1017	2	T30542	major surface glyc
39	62	13.4	1022	2	T30543	major surface glyc
40	62	13.4	1634	2	E64410	DNA-directed DNA p
41	61.5	13.3	409	2	H72669	probable N2,N2-dim
42	61.5	13.3	500	2	S22458	cellulase (EC 3.2.
43	61.5	13.3	516	2	S28060	serum response fac
44	61.5	13.3	668	2	C96501	hypothetical prote
45	61.5	13.3	887	2	T39492	conserved hypothet

ALIGNMENTS

RESULT 1
AE1734
anti-repressor homolog lin2418 [imported] - Listeria innocua (strain Clp11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1734
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla.
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1734
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97645.1; PID:gl6414940; GSPDB:GN00178
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin2418

Query Match 15.2%; Score 70; DB 2; Length 256;
Best Local Similarity 31.4%; Pred. No. 5.6;
Matches 16; Conservative 8; Mismatches 13; Indels 14; Gaps 1;
QY 27 ENGYLESRNKNHSQPTQSSLEDVTPPK-----AVKTKGK 63
DB 190 QNGYLISRRGTDYNRPTQKSMELGLFKIKETAIMRSSGAHTAITAKVTGK 240

RESULT 2
S76967
hypothetical protein - Synchocystis sp. (strain PCC 6803)
C:Species: Synchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocys
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <KAN>
A:Cross-references: EMBL:D64005; GB:AB001339; NID:gl001779; PIDN:BAAL0659.1; PID:d101
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 14.8%; Score 68.5; DB 2; Length 495;
Best Local Similarity 32.3%; Pred. No. 17;
Matches 20; Conservative 7; Mismatches 26; Indels 9; Gaps 2;

QY 21 SGNSTLENGYFLSRNKE-----NHQPTQSSLEDSVPTTKAVKTTG-KGIYKGRNLD 71
DB 23 SGTSTPTTGVIIAEVGEQAGASTEINQESNQKPGETKVNPLKVSATGVSVAKGKNGV 82

QY 72 SR 73
DB 83 LR 84

RESULT 3
A34549
transferrin receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: A34549
R:Roberts, K.P.; Griswold, M.D.
Mol. Endocrinol. 4, 531-542, 1990
A:Title: Characterization of rat transferrin receptor cDNA: the regulation of transferrin
A:Reference number: A34549; MUID:91125359; PMID:2126342
A:Accession: A34549
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-622 <NO>
A:Cross-references: GB:M58040; NID:9207463; PIDN:AAA42273.1; PID:9207464
C:Superfamily: transferrin receptor
C:Keywords: receptor; transmembrane protein

Query Match 14.8%; Score 68.5; DB 2; Length 622;
Best Local Similarity 27.6%; Pred. No. 22; Mismatches 15; Gaps 3;
Matches 21; Conservative 15; Indels 17; Gaps 3;

QY 32 LSRNKENHQSPT---QSSLEDSVPTTKAVKTTGK-----GIVKGRNLDLRGLI 76
DB 207 LFKNMEGNCPPSWNDSSCKLELSQNVKLTIVNVLKETRIINIFGVIKGYEEDRYIV 266

QY 77 LGA--EAWRGVKKNT 90
DB 267 VQAQRDAWPGVAKSS 282

RESULT 4
E82099
phosphatidate cytidyltransferase VC2255 [imported] - Vibrio cholerae (strain N16961 se
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82099
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Claydon, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.N.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82099
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-280 <HEI>
A:Cross-references: GB:AE004297; GB:AE003852; NID:99566810; PIDN:AAF95399.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2255
A:Map position: 1
C:Superfamily: phosphatidate cytidyltransferase

Query Match 14.7%; Score 68; DB 2; Length 280;
Best Local Similarity 25.3%; Pred. No. 10;
Matches 20; Conservative 17; Mismatches 20; Indels 22; Gaps 4;

QY 8 LLLAVCAIRNSGNTLENGYFLSRNKENHQSPTQSSLEDSVPTTKAVKTTGKIVYK 67

Db 151 LVLVFCFLVWADSGA-----YFVGKSLGKH-----KNAPAVSPNKTIEGLVGGIV-- 196

QY 68 RNLDSTRGLILG---AEAWG 83

Db 197 -----TAMLVGYWVAECFG 210

RESULT 5
T41524
rhol gdp-gtp exchange protein 1 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 23-Sep-2002
C:Accession: T41524
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z22000
A:Accession: T41524
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1334 <WOO>
A:Cross-references: EMBL:AL049498; PIDN:CAH39903.1; GSPDB:GN00069; SPDB:SPCC645.07
A:Experimental source: strain 972h; cosmid c645
C:Genetics:
A:Gene: SPDB:SPCC645.07
A:Map position: 3
A:Introns: 894/3
C:Superfamily: GDP/GTP exchange protein ROM1; CDC24 homology

Query Match 14.7%; Score 68; DB 2; Length 1334;
Best Local Similarity 21.8%; Pred. No. 59;
Matches 12; Conservative 19; Mismatches 22; Indels 2; Gaps 1;

QY 17 WRSNGSNTLENGYFLSRNKENHQSPTQSSLEDSVPTTKAVKTTGKIVKGRNLD 71
DB 152 WHTSGDDSNQNPFFVRKRSQSSSTSPVSDVDENL--LSAVSSVTESVETNLHLD 204

RESULT 6
A83026
hypothetical protein PA4966 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83026
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
; Loxy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83026
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-337 <STO>
A:Cross-references: GB:AE004909; GB:AE004091; NID:9951241; PIDN:AAG08351.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4966

Query Match 14.4%; Score 66.5; DB 2; Length 337;
Best Local Similarity 25.7%; Pred. No. 18;
Matches 19; Conservative 12; Mismatches 32; Indels 11; Gaps 2;

QY 15 AIWRNSGNTLENGYFLSRNKENHQSPTQSSLEDSVPTT-----KAVKTTGKIV 65
DB 55 ALWTVSDRDD--DRLYLQPSAEGSDQPAEASFIAPTPDGLPQWGMSTRVWLSGLV 112

QY 66 KGRNLDSTRGLILGA 79
DB 113 RGGNLDFFEGIACTA 126

RESULT 7
S41015

Query Match 14.8%; Score 68.5; DB 2; Length 495;
Best Local Similarity 32.3%; Pred. No. 17;
Matches 20; Conservative 7; Mismatches 26; Indels 9; Gaps 2;

QY 21 SGNSTLENGYFLSRNKE-----NHQPTQSSLEDSVPTTKAVKTTG-KGIYKGRNLD 71
DB 23 SGTSTPTTGVIIAEVGEQAGASTEINQESNQKPGETKVNPLKVSATGVSVAKGKNGV 82

QY 72 SR 73
DB 83 LR 84

RESULT 3
A34549
transferrin receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: A34549
R:Roberts, K.P.; Griswold, M.D.
Mol. Endocrinol. 4, 531-542, 1990
A:Title: Characterization of rat transferrin receptor cDNA: the regulation of transferrin
A:Reference number: A34549; MUID:91125359; PMID:2126342
A:Accession: A34549
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-622 <NO>
A:Cross-references: GB:M58040; NID:9207463; PIDN:AAA42273.1; PID:9207464
C:Superfamily: transferrin receptor
C:Keywords: receptor; transmembrane protein

Query Match 14.8%; Score 68.5; DB 2; Length 622;
Best Local Similarity 27.6%; Pred. No. 22; Mismatches 15; Gaps 3;
Matches 21; Conservative 15; Indels 17; Gaps 3;

QY 32 LSRNKENHQSPT---QSSLEDSVPTTKAVKTTGK-----GIVKGRNLDLRGLI 76
DB 207 LFKNMEGNCPPSWNDSSCKLELSQNVKLTIVNVLKETRIINIFGVIKGYEEDRYIV 266

QY 77 LGA--EAWRGVKKNT 90
DB 267 VQAQRDAWPGVAKSS 282

RESULT 4
E82099
phosphatidate cytidyltransferase VC2255 [imported] - Vibrio cholerae (strain N16961 se
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82099
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Claydon, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.N.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82099
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-280 <HEI>
A:Cross-references: GB:AE004297; GB:AE003852; NID:99566810; PIDN:AAF95399.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2255
A:Map position: 1
C:Superfamily: phosphatidate cytidyltransferase

Query Match 14.7%; Score 68; DB 2; Length 280;
Best Local Similarity 25.3%; Pred. No. 10;
Matches 20; Conservative 17; Mismatches 20; Indels 22; Gaps 4;

QY 8 LLLAVCAIRNSGNTLENGYFLSRNKENHQSPTQSSLEDSVPTTKAVKTTGKIVYK 67

transcription factor tbx8 - Caenorhabditis elegans

N:Alternate names: hypothetical protein T07C4.2

C:Species: Caenorhabditis elegans

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: S41015; A56530

R:Berks, M.

submitted to the EMBL Data Library, January 1994

A:Reference number: S41014

A/Accession: S41015

A/Molecule type: DNA

A/Residues: 1-479 <BER>

A/Cross-references: EMBL:Z29443

R:Agulnik, S.I.; Bollag, R.J.; Silver, L.M.

Genomics 25, 214-219, 1995

A>Title: Conservation of the T-box gene family from Mus musculus to Caenorhabditis elegans

A/Reference number: A56530; MUID:95293375; PMID:7774921

A/Accession: A56530

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 153-340 <AGU>

A/Cross-references: GB:Z29443

C/Genetics: 77/3; 101/3; 134/3; 236/2; 261/3; 312/3; 450/3

C/Introns: 77/3; 101/3; 134/3; 236/2; 261/3; 312/3; 450/3

C/Superfamily: Caenorhabditis elegans transcription factor tbx8; T-box homology

C/Keywords: DNA binding

F:153-340/Domain; T-box homology <TBX>

Query Match

Best Local Similarity 14.4%; Score 66.5; DB 1; Length 479;

Matches 18; Conservative 13; Mismatches 22; Indels 19; Gaps 3;

QY 19 SNSGNTLENGYFLSRNKHNSOPTQSSLEDSVTPTKAVKTTGKIVKGRNLDNRGLILG 78

DB 85 AHGASNT-----NKINQNLSP-HPAKHKTTIPSTVATVRGPPSGR-----126

QY 79 AEAWGRGVKNT 90

DB 127 -QEWGRGIQRT 137

RESULT 8

T47495

hypothetical protein F9K21.130 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C/Accession: T47495

R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.

submitted to the Protein Sequence Database, February 2000

A/Reference number: Z24467

A/Accession: T47495

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-851 <QOR>

A/Cross-references: EMBL:AL138657

A/Experimental source: cultivar Columbia; BAC clone F9K21

C/Genetics:

A/Map position: 3

A/Note: F9K21.130

Query Match

Best Local Similarity 14.3%; Score 66; DB 2; Length 851;

Matches 20; Conservative 13; Mismatches 23; Indels 22; Gaps 2;

QY 16 IWRSNS-GSNTLENGYFLSRNKHNSOPTQSSLEDSV-----TP 53

DB 625 IWSYNTGDTYVRSGLSTHDSPTTPTAKPHGSVDLTKTWNLPIMPKLKHLWRL 684

QY 54 TKAVKTTGKIVKGRNLD 71

DB 685 SKALPTDRLTLTRGMRID 702

RESULT 9

A82436

transcription regulator lysR family VCA0635 [imported] - Vibrio cholerae (strain N169

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C/Accession: A82436

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: A82436

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-313 <HEI>

A/Cross-references: GB:AE004393; GB:AE003853; NID:95658042; PIDN:AAF96536.1; GSPDB:GN

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics:

A/Gene: VCA0635

A/Map position: 2

C/Superfamily: conserved hypothetical protein HI1364

Query Match

Best Local Similarity 14.1%; Score 65; DB 2; Length 313;

Matches 23; Conservative 8; Mismatches 23; Indels 6; Gaps 3;

QY 23 SNTLENGYFLSRNKHNS--OPTQSSLEDSVTPTKAVKTTGKIVKGRNLD-SRGLILG 78

DB 196 ADTLHNKWLISRNGETHSVVQGNFACNDGEVHRLAVK--GKIANKSLMDSIIDIG 253

RESULT 10

H97313

protein distantly similar to N-terminal truncated of HSP60 chaperonin family [imported]

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C/Accession: H97313

R:Nolling, J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A/Reference number: A96900; MUID:21359325; PMID:21359325

A/Accession: H97313

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-360 <KUR>

A/Cross-references: GB:AE001437; PIDN:AAK81299.1; PID:gl5026451; GSPDB:GN00168

A/Experimental source: Clostridium acetobutylicum ATCC824

C/Genetics:

A/Gene: CAC3367

Query Match

Best Local Similarity 14.1%; Score 65; DB 2; Length 360;

Matches 22; Conservative 18; Mismatches 21; Indels 14; Gaps 5;

QY 19 SNSGNTLENGYFLSRNKHNSOPTQSSLEDSVTPTKAVKTT-----GKGIKGRNLDNR 73

DB 246 SHFGSDFAKGSFYLSEKMGYNPSE-----ITP-KAIKDIKKKWKQGIKAFKAKNK 298

QY 74 GLILGAWMGRGVKK 88

DB 299 G-IVGAEG-QNGIKK 311

RESULT 11

S36576

E2 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C/Accession: S36576

R:Deilius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

```
A;Reference number: S36469
A;Accession: S36576
A;Molecule type: DNA
A;Residues: 1-368 <DEL>
A;Cross-references: EMBL:X74481; NID:g3397038; PIDN:CAAS2588.1; PID:g3397042
C;Superfamily: papillomavirus E2 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 14.1%; Score 65; DB 2; Length 368;
Best Local Similarity 27.0%; Pred. No. 29;
Matches 24; Conservative 11; Mismatches 40; Indels 14; Gaps 3;

QY 10 LALVCEALWNSGNTLENGYFLSRN-----KENHSOPTQSSLEDSVTPTKAVK 58
Db 192 VIVCPASVSNEVSTT-ETAVHLCTSTKTSVAVGAKDTHLQPPQRRRPDVDSRNTK 250

QY 59 TTQGVKIVGNLDS--RGILGAEAWGRG 85
Db 251 YPNLLRGQGVSDTTRGLVTATECTNKG 279

RESULT 12
T24654
hypothetical protein T07D10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T24654
R;White, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19918
A;Accession: T24654
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-379 <WIL>
A;Cross-references: EMBL:Z81588; PIDN:CAB04712.1; GSPDB:GN00019; CESP:T07D10.2
A;Experimental source: clone T07D10
C;Genetics:
A;Gene: CESP:T07D10.2
A;Map position: 1
A;Introns: 37/3; 85/3; 271/1; 319/1
C;Superfamily: oxytocin receptor

Query Match 14.1%; Score 65; DB 2; Length 379;
Best Local Similarity 35.9%; Pred. No. 30;
Matches 14; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 8 LLLLVCAIWRNSGNTLENGYFLSRNKENHSOPTQSS 46
Db 228 LYLVCCKAVWKSTSFSSSLRN----NMKKMEHMKLTKN 262

RESULT 13
T06029
hypothetical protein T28I19.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06029
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15484
A;Accession: T06029
A;Molecule type: DNA
A;Residues: 1-532 <BEV>
A;Cross-references: EMBL:AL035709; GSPDB:GN00062; ATSP:T28I19.100
A;Experimental source: cultivar Columbia; BAC clone T28I19
C;Genetics:
A;Gene: ATSP:T28I19.100
A;Map position: 4

Query Match 14.0%; Score 64.5; DB 2; Length 532;
Best Local Similarity 34.7%; Pred. No. 50;
Matches 17; Conservative 9; Mismatches 18; Indels 5; Gaps 1;

QY 14 EAINWNSGNTLENGYFLSRNKENHSOPTQSSLEDSVTPTKAVKTTGK 62
Db 274 ESSGDSGSGKSTGYOQTKNEDEKVKQSSSEES-----KVESGK 317

RESULT 14
A11442
anti-repressor (Bacteriophage A118) homolog lin0080 [imported] - Listeria innocua (st.
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: A11442
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <GLA>
A;Cross-references: GB:ALS92022; PIDN:CAC95313.1; PID:g16412500; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0080

Query Match 13.9%; Score 64; DB 2; Length 257;
Best Local Similarity 29.4%; Pred. No. 25;
Matches 15; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 27 ENGYSFLSRNKENHSOPTQSSLEDSVTPTK-----AVKTTGKG 63
Db 191 QRGYLIRKGTIDYNRPTQKSMELGLFKIKETAIIRSSGQTAITAKVTGK 241

RESULT 15
T46099
hypothetical protein T25B15.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 06-Oct-2000
C;Accession: T46099
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23021
A;Accession: T46099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <ALC>
A;Cross-references: EMBL:AL132972
A;Experimental source: cultivar Columbia; BAC clone T25B15
C;Genetics:
A;Map position: 3
A;Introns: 23/3; 122/3; 194/3; 234/3
A;Note: T25B15.60
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L24.240

Query Match 13.9%; Score 64; DB 2; Length 430;
Best Local Similarity 27.4%; Pred. No. 45;
Matches 20; Conservative 14; Mismatches 23; Indels 16; Gaps 3;

QY 17 WRSNS--GSNT-----LENGYFLSRNKENHSOPTQSSLEDSVTPTKAVKTTG 61
Db 237 WKNSTKMGSGQTFMDPNPNHGWHSWLER-WWAAPNENHSUTPDNAEKDSSARSVASRAMS 295

QY 62 KGIVKGNLDSRG 74
Db 296 EMIPRGKNLSPRG 308

Search completed: March 31, 2004, 12:15:28
Job time : 22 secs
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:12:31 ; Search time 23 Seconds
(without alignments)
202.015 Million cell updates/sec

Title: US-09-989-293A-377
Perfect score: 462
Sequence: 1 MTFLLSLLLLLVCEAIRNSN.....DSRGLILGAEAWGRGVKXNT 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A COMB pep.*
2: /cgn2_6/prodata/2/iaa/5B COMB pep.*
3: /cgn2_6/prodata/2/iaa/6A COMB pep.*
4: /cgn2_6/prodata/2/iaa/6B COMB pep.*
5: /cgn2_6/prodata/2/iaa/PTUS COMB pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	143.5	31.1	244	US-08-772-440-2	Sequence 2, Appli
2	139.5	30.2	50	US-08-772-440-25	Sequence 25, Appl
3	139.5	30.2	176	US-08-772-440-8	Sequence 8, Appli
4	128.5	27.8	180	US-08-772-440-31	Sequence 31, Appl
5	69.5	15.0	171	US-09-205-258-481	Sequence 481, App
6	69.5	15.0	257	US-09-205-258-421	Sequence 421, App
7	68.5	14.8	622	US-08-547-197-1	Sequence 1, Appli
8	68.5	14.8	622	US-08-957-940-1	Sequence 1, Appli
9	66.5	14.4	354	US-09-252-991A-32891	Sequence 32891, A
10	65.5	14.2	247	US-09-134-000C-6345	Sequence 6345, Ap
11	65	14.1	461	US-09-134-001C-3604	Sequence 3604, Ap
12	64	13.9	126	US-09-198-452A-1254	Sequence 1254, Ap
13	63.5	13.7	317	US-09-594-506-30	Sequence 30, Appl
14	63.5	13.7	881	US-09-489-039A-12003	Sequence 12003, A
15	63	13.6	315	US-09-134-001C-4255	Sequence 4255, Ap
16	62	13.4	1017	US-09-762-724-12	Sequence 12, Appl
17	62	13.4	1023	US-09-762-724-14	Sequence 14, Appl
18	62	13.4	1027	US-09-762-724-8	Sequence 8, Appli
19	61.5	13.3	789	US-08-960-780-6	Sequence 6, Appli
20	61.5	13.3	789	US-03-073-898-6	Sequence 6, Appli
21	61.5	13.3	789	US-09-002-285-90	Sequence 90, Appl
22	61.5	13.3	789	US-09-589-477-90	Sequence 90, Appl
23	61.5	13.3	789	US-09-850-351A-6	Sequence 6, Appli
24	61	13.2	237	US-08-808-148-3	Sequence 3, Appli
25	61	13.2	237	US-08-976-594-216	Sequence 216, App
26	61	13.2	254	US-09-252-991A-21292	Sequence 21292, A
27	60	13.0	217	US-09-107-532A-6400	Sequence 6400, Ap

28	60	13.0	1029	4	US-09-762-724-6	Sequence 6, Appli
29	59.5	12.9	237	4	US-09-252-991A-26577	Sequence 26577, A
30	59.5	12.9	921	4	US-09-543-681A-5734	Sequence 5734, Ap
31	59	12.8	415	4	US-03-252-991A-31892	Sequence 31892, A
32	59	12.8	641	3	US-08-836-567-10	Sequence 10, Appl
33	59	12.8	641	4	US-09-606-304-10	Sequence 4, Appli
34	59	12.8	1742	4	US-09-386-962C-4	Sequence 2, Appli
35	59	12.8	3623	4	US-09-341-461-2	Sequence 4, Appli
36	58.5	12.7	418	3	US-09-030-267-5	Sequence 5, Appli
37	58.5	12.7	924	3	US-08-619-812-8	Sequence 2, Appli
38	58.5	12.7	926	1	US-07-908-253-2	Sequence 2, Appli
39	58.5	12.7	926	1	US-08-455-970A-2	Sequence 2, Appli
40	58.5	12.7	926	1	US-08-387-156-6	Sequence 6, Appli
41	58.5	12.7	926	2	US-08-694-865-6	Sequence 6, Appli
42	58.5	12.7	926	2	US-08-878-748-6	Sequence 2, Appli
43	58.5	12.7	926	2	US-08-535-837-2	Sequence 2, Appli
44	58.5	12.7	926	3	US-09-124-431-6	Sequence 6, Appli
45	58.5	12.7	926	4	US-09-383-912-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-772-440-2
; Sequence 2, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTDX:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-772-440-2

Query Match 31.1%; Score 143.5; DB 3; Length 244;
Best Local Similarity 61.7%; Pred. No. 7.6e-10;
Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;
Qy 15 AIWRNSGNTLENGVLSNKENHSQPTOSLSLDSVTPTKAVKTTG 61
Db 68 AFWRHNSGRNPFKNFLSRNKNH-KPTESLSLDEKVPKASQTTG 113

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; US-08-772-440-8
;
; Query Match 30.2%; Score 139.5; DB 3; Length 176;
; Best Local Similarity 62.2%; Pred. No. 1.5e-09;
; Matches 28; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
;
; QY 17 WRNSGNTLENGYFLSRKNHNSOPTQSSLEDSVPTKAVKTTG 61
; Db 2 WRNSGRNPEKDNFLSRKNH-KPTSSLDKVPKSKASQTIG 45
;
; RESULT 4
; US-08-772-440-31
; Sequence 31, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-772-440-25
;
; Query Match 30.2%; Score 139.5; DB 3; Length 50;
; Best Local Similarity 62.2%; Pred. No. 2.6e-10;
; Matches 28; Conservative 6; Mismatches 10; Indels 1; Gaps 1;
;
; QY 17 WRNSGNTLENGYFLSRKNHNSOPTQSSLEDSVPTKAVKTTG 61
; Db 2 WRNSGRNPEKDNFLSRKNH-KPTSSLDKVPKSKASQTIG 45
;
; RESULT 3
; US-08-772-440-8
; Sequence 8, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-772-440-31
;
; Query Match 27.8%; Score 128.5; DB 3; Length 180;

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Best Local Similarity 62.8%; Pred. No. 3.7e-08;
Matches 27; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 19 SNSGNTLNGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTG 61
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 8 SNSGRNPEKDFLSRKNENH-KPTLESSLDERKVPKASQTG 49

RESULT 5
US-09-205-258-481
; Sequence 481, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 481
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-205-258-481

Query Match 15.0%; Score 69.5; DB 4; Length 171;
Best Local Similarity 31.8%; Pred. No. 0.8;
Matches 21; Conservative 14; Mismatches 22; Indels 9; Gaps 2;

QY 5 LSLILLVCEA---IWRNSGNTLNGYFLSRN-----KENHSQPTQSSLEDSVTPTK 55
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 25 LVALLLVSAALSSVSVSRDPSPTVLNHSITPNVNALTHEQTKEPSISQISTLTLPPTI 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 56 AVKTTG 61
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Db 85 STKKG 90

RESULT 6
US-09-205-258-421
; Sequence 421, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06

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; SEQ ID NO 421
; LENGTH: 257
; TYPE: PAT
; ORGANISM: Homo sapiens
US-09-205-258-421

Query Match      15.0%; Score 69.5; DB 4; Length 257;
Best Local Similarity 31.8%; Pred. No. 1.4;
Matches 21; Conservative 14; Mismatches 22; Indels 9; Gaps 2;

QY 5 LSLILLVCEA-----IWRNSGNSVLENGYFYSRN-----KENHSQPTOSLSLDSVTPTK 55
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 LVLALLNSAALS SVVSRDTSPTVLASHSTPNVNLATHENQTKPSISQISTTILPPTT 84
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 AVKTTG 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 STKSG 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-08-547-197-1
; Sequence 1, Application US/08547197
; Patent No. 5691157
; GENERAL INFORMATION:
; APPLICANT: Gong, Joseph K.
; APPLICANT: Glowski, Chester A.
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/547,197
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rogalsky, Peter
; REGISTRATION NUMBER: 38,601
; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1634
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-547-197-1

Query Match      14.8%; Score 68.5; DB 1; Length 622;
Best Local Similarity 27.6%; Pred. No. 6.4;
Matches 21; Conservative 15; Mismatches 23; Indels 17; Gaps 3;

QY 32 LSRKNENHSQPT---QSSLEDSVTPTKAVTKTGK-----GIVKGRNLDSRLGI 76
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 207 LFKMNEGNCPSWIDSSKLELSONQNVKLTVNVLKETILNIFGVIKGYEEDRIV 266
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 77 LGA--EAWGRGVKXNT 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 VQAQDANGPGVAKSS 282
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
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; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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Mon Apr 5 12:01:58 2004

RESULT 8
US-08-957-940-1
; Sequence 1, Application US/08957940
; Patent No. 6132981
; GENERAL INFORMATION:
; APPLICANT: Gong, Joseph K.
; APPLICANT: Glomski, Chester A.
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,940
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/547,197
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rogalsky, Peter
; REGISTRATION NUMBER: 36,601
; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1634
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-957-940-1

Query Match 14.8%; Score 68.5; DB 3; Length 622;
Best Local Similarity 27.6%; Pred. No. 6.4;
Matches 21; Conservative 15; Mismatches 23; Indels 17; Gaps 3;

Qy 32 LSRNKHNSQPT---QSSLEDSVPTTKAVKTKG-----GIVKGNLDSGLI 76
Db 207 LFKMNEGCPSPWNIDSSCKELSONQNVKLTNNVLKETRLNIFGVKGYEEDRYIV 265
Qy 77 LGA--EAWGRGVKXNT 90
Db 267 VGAQRDANGPGVAKSS 282

RESULT 9
US-09-252-991A-32891
; Sequence 32891, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32891
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32891

Query Match 14.4%; Score 66.5; DB 4; Length 354;
Best Local Similarity 25.7%; Pred. No. 5.2;
Matches 19; Conservative 12; Mismatches 32; Indels 11; Gaps 2;

Qy 15 AIWRNSGNTLENGYFLSRNKHNSQPTQSSLEDSVPT-----KAVKTKGKIV 65
Db 72 ALWTVSDRDD--DRYLRLQPSAEGSDQFWQAESEFIAPTDPDSGLPQWGMSTRVWLSGLV 129
Qy 66 KGRNLDSEGLIIGA 79
Db 130 RGNLDFEGIACDA 143

RESULT 10
US-09-134-000C-6345
; Sequence 6345, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 6345
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6345

Query Match 14.2%; Score 65.5; DB 4; Length 247;
Best Local Similarity 30.8%; Pred. No. 4.2;
Matches 16; Conservative 7; Mismatches 14; Indels 15; Gaps 1;

Qy 27 ENGYFLSRNKHNSQPTQSSLEDSVPTTKAVKTKG 63
Db 185 EGYLIKRRKGTDMNPTQKSMDLFEVKETIARSDGSYSISKTPKVTCKG 236

RESULT 11
US-09-134-001C-3604
; Sequence 3604, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3604
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3604

Query Match 14.1%; Score 65; DB 4; Length 461;
Best Local Similarity 29.5%; Pred. No. 12;
Matches 18; Conservative 10; Mismatches 19; Indels 14; Gaps 3;

QY 23 SNTLENGY-FLSRN-----KENH-----SQTQSSLEDSVTPTKAVKTTGKGVKGR 68
DB 83 SNVHPGFGFLSESTNFAKAVEDNHLHFGPSKTTWMMGDKITARQIVKQAGVPVPGS 142

QY 69 N 69
DB 143 N 143

RESULT 12
US-09-198-452A-1254
; Sequence 1254, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1254
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1254

Query Match 13.9%; Score 64; DB 4; Length 126;
Best Local Similarity 24.8%; Pred. No. 2.5;
Matches 25; Conservative 14; Mismatches 30; Indels 32; Gaps 4;

QY 6 SLLLLVCEAIRWSNGSNTLENGYFLSRN---KENHSQ-----TQSSLEDSVT 52
DB 15 AICLASCSKV-----SSRFLSNINFKNTTTPREIVLIPNPTMSALNPEIT 63

QY 53 P-----TKAVKTTGKGVKGRNLDRLGILGAEAWGRG 85
DB 64 PLSTIAPQTRRPTTKVTPRARDLLSLGITNFVSSGGVG 104

RESULT 13
US-09-594-506-30
; Sequence 30, Application US/09594506
; Patent No. 6512164
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Thiamine Biosynthetic Enzymes
; FILE REFERENCE: BB1372 US NA
; CURRENT APPLICATION NUMBER: US/09/594,506
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,556
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-594-506-30

Query Match 13.7%; Score 63.5; DB 4; Length 317;
Best Local Similarity 24.2%; Pred. No. 11;
Matches 23; Conservative 20; Mismatches 33; Indels 19; Gaps 4;

QY 10 LLVCEAIRWSNGSNTLENGYFLSRNKHNSQPTQSSLEDSVTPTKAV-----KT 59
DB 163 VVVEDLVVKEHRTGVVTNVALSVNQDTHSQ-TQSHMDANVMEAKIVVSSCGHGLFSA 221

QY 60 TGKGVKGRNLDRLGLJ-----LGAEAWGRGVKKN 89
DB 222 NGKGV---KRLDGLMIKTVPTGRTGNEALDITNVED 253

RESULT 14
US-09-489-039A-12003
; Sequence 12003, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12003
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12003

Query Match 13.7%; Score 63.5; DB 4; Length 881;
Best Local Similarity 29.9%; Pred. No. 44;
Matches 20; Conservative 7; Mismatches 29; Indels 11; Gaps 2;

QY 17 WRSNSGNTLENGYFLSRNKHNSQPTQSSLEDSVTPTKAVKTTGKGVKGRNLD---R 73
DB 234 WSYSSGGSTSSN-----ENRQWQVNSWLERDITPLRSRLTLGDSYTNQGVDFDGINFR 285

QY 74 GLILGAE 80
DB 286 GAQLASD 292

RESULT 15
US-09-134-001C-4255
; Sequence 4255, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4255
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4255

Query Match 13.6%; Score 63; DB 4; Length 315;
Best Local Similarity 28.6%; Pred. No. 12;
Matches 22; Conservative 12; Mismatches 35; Indels 8; Gaps 2;

QY 12 VCEAIRWSNGSNTLENGYFLSRNKHNSQPTQSSLEDSVTPT---KAVKTTGKGVKGRN 69
DB 146 VIDPWLAKSGDSLMD-----ENTKNHLQSLTLLPLADVVTNPIPEAEITGKINDEES 199

QY 70 LDSGLILGAEAWGRGV 86
DB 200 IRKAGQIFINEIGSKGV 216

Mon Apr 5 12:01:58 2004

us-09-989-293a-377.rai

Page 7

Search completed: March 31, 2004, 12:16:02
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:11:11 ; Search time 39 Seconds
(without alignments)
728.119 Million cell updates/sec

Title: US-09-989-293A-377
Perfect score: 462
Sequence: 1 MTFLLSLLLVCEAIWRSN.....DSRGLILGAEAWGRGVKNT 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247.5	53.6	189	Q96DR9	Q96dr9 homo sapien
2	247.5	53.6	192	Q96PA5	Q96pa5 homo sapien
3	247.5	53.6	247	Q9BXN2	Q9bxn2 homo sapien
4	217.5	47.1	247	Q9H2R8	Q9h2r8 macaca mula
5	143.5	31.1	244	Q9J750	Q9ji50 mus musculus
6	136.5	29.5	244	Q8K1L4	Q8kl14 mus musculus
7	80	17.3	239	Q8NZP4	Q8nzp4 streptococc
8	80	17.3	242	Q938N5	Q938n5 streptococc
9	78	16.9	238	O48391	O48391 streptococc
10	77	16.7	287	Q38585	Q38585 streptococc
11	75	16.2	217	Q8S2U4	Q8s2u4 medicago sa
12	71	15.4	213	Q9SBR7	Q9sbr7 medicago va
13	70	15.2	205	Q8PDR9	Q8pdr9 xanthomonas
14	70	15.2	256	Q928W4	Q928w4 listeria in
15	70	15.2	661	Q9VG84	Q9vg84 drosophila
16	70	15.2	696	Q8MZC0	Q8mzc0 drosophila

17	69.5	15.0	265	4	Q8NC54
18	69.5	15.0	265	4	Q5NRG2
19	68.5	14.8	495	16	Q55897
20	68.5	14.8	498	13	Q33291
21	68	14.7	280	16	Q9KEV7
22	68	14.7	1008	16	Q8FA78
23	68	14.7	1334	3	Q9Y7U6
24	67.5	14.6	417	10	Q8LAR3
25	67	14.5	150	11	Q9D851
26	67	14.5	321	11	Q8BTR4
27	67	14.5	356	13	O57435
28	67	14.5	975	5	Q862D2
29	67	14.5	976	5	Q8INT1
30	66.5	14.4	337	16	Q9HUJ9
31	66.5	14.4	602	10	Q8W3H4
32	66.5	14.4	602	10	Q7XBV7
33	66	14.3	145	12	Q8AZ84
34	66	14.3	145	12	Q8AZ83
35	66	14.3	145	12	Q8AZ82
36	66	14.3	145	12	Q8AZ81
37	66	14.3	145	12	Q8AZ80
38	66	14.3	260	12	Q919W1
39	66	14.3	417	10	Q9SFE3
40	66	14.3	491	12	Q919W0
41	66	14.3	491	12	Q919W2
42	66	14.3	498	12	Q9YIL3
43	66	14.3	498	12	Q9QNB5
44	66	14.3	498	12	Q8QM08
45	66	14.3	498	12	Q9QN84

ALIGNMENTS

RESULT 1

Q96DR9 PRELIMINARY; PRT; 189 AA.

AC Q96DR9; (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-glucan receptor isoform C.

GN BGR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood leukocytes;

RA Willment J.A., Gordon S., Brown G.D.;

RT "Characterization of the human beta-glucan receptor and its alternatively spliced isoforms."

RL J. Biol. Chem. 0:0-0(2001).

DR EMBL; AF400597; AAL1713.1; -

DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.

SQ SEQUENCE. 189 AA; 21065 MW; F7DF9F76EA4B6B59 CRC64;

Query Match 53.6%; Score 247.5; DB 4; Length 189;
Best Local Similarity 80.6%; Pred. No. 5.8e-19;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

Qy	5	LSLLLLVC-----EAIWRNSGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKT	59
Db	53	LCILVILVAVLGTMAIWRNSGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKT	112
Qy	60	TG 61	
Db	113	TG 114	

RESULT 2

Q96PA5 Q96PA5 PRELIMINARY; PRT; 192 AA.
AC Q96PA5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucan receptor isoform G.
GN BGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta-glucan receptor and its
alternatively spliced isoforms.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF400601; AAL11717.1;
DR GO; GO:0004872; F:receptor activity; IEA.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 192 AA; 21130 MW; 6F3350B1DFBEC921 CRC64;
Query Match 53.6%; Score 247.5; DB 4; Length 192;
Best Local Similarity 80.6%; Pred. No. 5.9e-19;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;
QY 5 LSLALLLVC-----EAIWRSNGSNTLENGYFLSRNKHNSQTSLSDSVTPTKAVKT 59
Db LCLVILVIAVLGTMAIWRSGNSNTLENGYFLSRNKHNSQTSLSDSVTPTKAVKT 112
QY 60 TG 61
Db 113 TG 114
RESULT 3
Q9BXN2 Q9BXN2 PRELIMINARY; PRT; 247 AA.
AC Q9BXN2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dendritic cell-associated C-type lectin-1 (DECTIN-1 receptor) (Lectin-
like receptor 1) (Beta-glucan receptor isoform A).
GN DECTIN-1 OR DECTIN1 OR BGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;
RT "Identification of a human homologue of the dendritic cell-associated
C-type lectin-1, dectin-1.";
RL Gene 272:51-60(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Sobanov Y., Bernreiter A., Derdak S., Mechtcheriakova D., Duechler M.,
RA Kalthoff F., Hofer E.;
RT "A novel cluster of lectin-like receptor genes expressed in monocytic,
dendritic and endothelial cells maps close to the NK receptor genes in
the human NK gene complex.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383615; PubMed=11491532;
RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
expressed on dendritic cells.";
RL Immunogenetics 53:288-295(2001).
RN [4]

RP SEQUENCE FROM N.A.
RA Herranz-Falcon P., Arce I., Fernandez-Ruiz E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood leukocytes;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta-glucan receptor and its
alternatively spliced isoforms.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF313468; AAK37473.1;
DR EMBL; AJ312373; CAC43847.1;
DR EMBL; AY026769; AAK20114.2;
DR EMBL; AF400595; AAL11711.1;
DR Genew; HGNC:14558; CLECSF12.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin; Receptor.
SQ SEQUENCE 247 AA; 27627 MW; 98393E3697611B9 CRC64;
Query Match 53.6%; Score 247.5; DB 4; Length 247;
Best Local Similarity 80.6%; Pred. No. 8.1e-19;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;
QY 5 LSLALLLVC-----EAIWRSNGSNTLENGYFLSRNKHNSQTSLSDSVTPTKAVKT 59
Db LCLVILVIAVLGTMAIWRSGNSNTLENGYFLSRNKHNSQTSLSDSVTPTKAVKT 112
QY 60 TG 61
Db 113 TG 114
RESULT 4
Q8HZR8 Q8HZR8 PRELIMINARY; PRT; 247 AA.
AC Q8HZR8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dendritic cell-associated C-type lectin-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi Y.K., Fallert B.A., Murphey-Corb M.A., Reinhart T.A.;
RT "Simian Immunodeficiency Virus Dramatically Alters Expression of
Homeostatic Chemokines and Dendritic Cell Markers during Infection In
Vivo.";
RL Blood 0:0-0(2002).
DR EMBL; AF508729; AAN47097.1;
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
SQ SEQUENCE 247 AA; 27648 MW; 9DF0D86DF2461518 CRC64;
Query Match 47.1%; Score 217.5; DB 6; Length 247;

DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C.1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;

Query Match 29.5%; Score 136.5; DB 11; Length 244;
Best Local Similarity 59.6%; Pred. No. 1e-06;
Matches 28; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 15 AIWRNSGNTLENGYFLSRNKENHSPQSSLEDSTVPTKAVKTG 61
DB 68 AFWRHNSGRNPEEKDNFSLRNKENH-KPTESLDEKVAPSKASOTTG 113

RESULT 7
QBNZP4 PRELIMINARY; PRT; 239 AA.
AC QBNZP4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical phage protein spym18_1802.
GN SPYM18_1802.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F., RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
RL EMBL; A010087; AAL98325.1; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; ANT; 1.
DR Complete proteome; Hypothetical protein.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 239 AA; 27449 MW; 91988787A84A9853 CRC64;

Query Match 17.3%; Score 80; DB 16; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.5;
Matches 19; Conservative 11; Mismatches 14; Indels 20; Gaps 2;

QY 20 NSGNTL-----ENGYFLSRNKENHSPQSSLEDSTVPTKAVKT 59
DB 162 NIGQNLFAWLRENGFLIRKNGESYNNFTQSRMDMKLFEVKERTHPNGSIRISKTKM 221

QY 60 TGKG 63
DB 222 TGRG 225

RESULT 8
Q38N5 PRELIMINARY; PRT; 242 AA.
ID Q38N5
AC Q38N5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Antirepressor (Putative P1-type antirepressor-phage associated).
GN SPYM3_1261 OR SP50602.
OS Streptococcus pyogenes, and Streptococcus pyogenes (serotype M3).

DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C.1.
DR PRINTS; PR00356; ANTI-FREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;

Query Match 29.5%; Score 136.5; DB 11; Length 244;
Best Local Similarity 59.6%; Pred. No. 1e-06;
Matches 28; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 15 AIWRNSGNTLENGYFLSRNKENHSPQSSLEDSTVPTKAVKTG 61
DB 68 AFWRHNSGRNPEEKDNFSLRNKENH-KPTESLDEKVAPSKASOTTG 113

RESULT 6
Q8K1L4 PRELIMINARY; PRT; 244 AA.
ID Q8K1L4
AC Q8K1L4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to C-type (calcium dependent, carbohydrate recognition domain)
DE lectin, superfamily member 12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC027742; AAH27742.1; -;
DR GO; GO:0005529; F:sugar binding; IEA.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN [1]_SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=NIH1;
RA Ikbe T., Wada A., Inagaki Y., Sugama K., Tanaka D., Suzuki R.,
RA Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.;
RT "Complete sequence of temperate phage PhiNH1.1";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN [3]
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [3]
RC SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, Sf370 and MGAS232";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050245; AAL15047.1; -
DR EMBL; AE014160; AAM79868.1; -
DR EMBL; AP005143; BAC63697.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 242 AA; 27843 MW; 5AA85551447E366C CRC64;

Query Match 17.3%; Score 80; DB 16; Length 242;
Best Local Similarity 35.9%; Pred. No. 1.5;
Matches 23; Conservative 5; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTKAV-KT 59
Db 163 NIGQNKLFQWLRNGYLLSRGSGWNPQTKSMQLGLFELKKTAINHSDGHTTTNTPKV 222
QY 60 TGKG 63
Db 223 TGKG 226

RESULT 9
O48391
ID O48391 PRELIMINARY; PRT; 238 AA.
AC O48391;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pl-antirepressor homolog.
OS Streptococcus thermophilus bacteriophage TP-J34.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=73422;
RN [1]
RN [2]
RC STRAIN=TP-J34;
RX MEDLINE=98122991; PubMed=9454717;
RA Neve H., Zenz K.I., Desiere F., Koch A., Heller K.J., Brussow H.;
RT "Comparison of the lysogeny modules from the temperate streptococcus
RT thermophilus bacteriophages TP-J34 and sfi21: implications for the
RT modular theory of phage evolution.";
RL Virology 241:61-72 (1998).

Query Match 16.7%; Score 77; DB 9; Length 287;
Best Local Similarity 34.4%; Pred. No. 3.9;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 208 NIGRNLFWLRNGYLLSRGSGWNPQTKSMQLGLFELKKTININHADGHTTTNTTKV 267
QY 60 TGKG 63
Db 268 TGKG 271

RESULT 11
Q8S2U4

DR EMBL; AF020798; AAC03459.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
SQ SEQUENCE 238 AA; 27081 MW; C30F3E9701BEE651 CRC64;

Query Match 16.9%; Score 78; DB 9; Length 238;
Best Local Similarity 34.4%; Pred. No. 2.4;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 159 NIGQNKLFQWLRNGYLLSRGSGWNPQTKSMQLGLFELKKTININHADGHTTTNTTKV 218
QY 60 TGKG 63
Db 219 TGKG 222

RESULT 10
Q38585
ID Q38585 PRELIMINARY; PRT; 287 AA.
AC Q38585;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ANTI-repressor protein.
GN ANTI.
OS Streptococcus thermophilus bacteriophage Sfi21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=64186;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96204576; PubMed=8623559;
RA Bruttin A., Brussow H.;
RT "Site-specific spontaneous deletions in three genome regions of a
RT temperate Streptococcus thermophilus phage.";
RL Virology 219:96-104 (1996).
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98160788; PubMed=9499809;
RA Desiere F., Lucchini S., Bruttin A., Brussow H.;
RT "Evolution of Streptococcus thermophilus bacteriophage genomes by
RT modular exchanges followed by point mutations and small deletions and
RT insertions.";
RL Virology 241:345-356 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Desiere F., Lucchini S., Bruttin A., Brussow H.;
RT "Streptococcus thermophilus bacteriophage Sfi21 complete genome.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95646; CAA64937.1; -
DR EMBL; AF115103; AAD44100.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
SQ SEQUENCE 287 AA; 33148 MW; 49651DA8F986CF50 CRC64;

Query Match 16.7%; Score 77; DB 9; Length 287;
Best Local Similarity 34.4%; Pred. No. 3.9;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 208 NIGRNLFWLRNGYLLSRGSGWNPQTKSMQLGLFELKKTININHADGHTTTNTTKV 267
QY 60 TGKG 63
Db 268 TGKG 271

RESULT 11
Q8S2U4

RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kref J., Kuhn M., Kunst F., Kurapat G.,
 RA Madueno E., Maitournam A., Mara Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo T., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Smoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of *Listeria species.*";
 RL Science 294:849-852(2001).
 RA EMBL: AL596172; CAC97645.1; -
 DR PIR: AE1734; AE1734.
 DR Lintlilist; LINC2418; -
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR005039; Anti_rep.
 DR InterPro: IPR003497; BRO_Nterm.
 DR Pfam: PF031374; ANT; 1.
 DR Pfam: PF02498; Bro-N; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 256 AA; 29082 MW; 5FE3FCEFC81A8B6 CRC64;
 Query Match 15.2%; Score 70; DB 16; Length 256;
 Best Local Similarity 31.4%; Pred. No. 20;
 Matches 16; Conservative 8; Mismatches 13; Indels 14; Gaps 1;
 QY 27 ENGFLRNKHNHQSSLEQSVTPK-----AVKTKGK 63
 Db 190 QNGYLISRRGTQYRNPQKSMELGLFKIKETAINRSSGAHTAIKATYTKGK 240
 RESULT 15
 Q9VG84
 ID Q9VG84 PRELIMINARY; PRT; 661 AA.
 AC Q9VG84;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG17227 protein (EC 6.5.1.1) (DNA ligase) (Polydeoxyribonucleotide
 DE synthase [ATP]).
 GN CG17227.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Franckoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny L., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster.*";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Ibegwam C., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Jbegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE) (N) +
 CC {DEOXYRIBONUCLEOTIDE} (M) = AMP + DIPHOSPHATE +
 CC {DEOXYRIBONUCLEOTIDE} (N+M).
 CC -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
 DR EMBL: AE003695; AAF54801.2; -
 DR FlyBase; FBgn0038035; CG17227.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0003910; F:DNA ligase (ATP) activity; IEA.
 DR GO: GO:0014874; F:ligase activity; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR GO: GO:0006281; P:DNA repair; IEA.
 DR GO: GO:0006260; P:DNA replication; IEA.
 DR InterPro; IPR000977; DNA_ligase.
 DR Pfam; PF01068; DNA_ligase; 1.
 DR Pfam; PF04579; DNA_ligase_A_C; 1.
 DR Pfam; PF04579; DNA_ligase_A_N; 1.
 DR TIGRfams; TIGR00574; dnll; 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; 1.
 DR PROSITE; PS00333; DNA_LIGASE_A2; 1.
 DR PROSITE; PS0160; DNA_LIGASE_A3; 1.
 KW ATP-binding; DNA recombination; DNA repair; DNA replication; Ligase.
 SQ SEQUENCE 661 AA; 73899 MW; 5C5711C0AF2D7F27 CRC64;

Query Match

15.2%; Score 70; DB 5; Length 661;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:07:20 ; Search time 54 Seconds
(without alignments)
470.913 Million cell updates/sec

Title: US-09-989-293A-377
Perfect score: 462
Sequence: 1 MTFFLSLLLLVCEAIWRSN.....DSRGLILGAEWGRGVKKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	90	3 AAY66748	Aay66748 Membrane-
2	462	100.0	90	3 AAB33469	Aab33469 Human PRO
3	462	100.0	90	4 AAU12408	Aau12408 Human PRO
4	462	100.0	90	4 AAB50922	Aab50922 Human PRO
5	462	100.0	90	4 AAB52711	Aab52711 Human PRO
6	462	100.0	90	6 ABUS8086	Abus8086 Human PRO
7	462	100.0	90	6 ABUS9164	Abus9164 Novel hum
8	462	100.0	90	6 ABUS2676	Abus2676 Human sec
9	462	100.0	90	6 ABO17852	Abol7852 Novel hum
10	462	100.0	90	6 ABUS60595	Abu60595 Human sec
11	462	100.0	90	6 ABU13977	Abu13977 Human PRO
12	462	100.0	90	6 ABUS91106	Abu91106 Human PRO
13	462	100.0	90	6 ABUS72562	Abu72562 Novel hum
14	462	100.0	90	6 ABUS6806	Abus6806 Human PRO
15	462	100.0	90	6 ABUS9887	Abus9887 Novel sec
16	462	100.0	90	6 ABUS9311	Abus9311 Human sec
17	462	100.0	90	6 ABO26008	Abol26008 Human PRO
18	462	100.0	90	6 ABO25077	Abol25077 Human sec
19	462	100.0	90	6 ABUS9017	Abus9017 Human sec
20	462	100.0	90	6 ABUS92395	Abus92395 Novel hum
21	462	100.0	90	6 ABUS9460	Abus9460 Novel hum
22	462	100.0	90	6 ABUS7082	Abus7082 Human sec
23	462	100.0	90	6 ABUS92226	Abus92226 Novel hum
24	462	100.0	90	6 ABU10932	Abu10932 Human PRO
25	462	100.0	90	6 ABUS1684	Abus1684 Novel hum

ALIGNMENTS

RESULT 1
AAY66748
ID AAY66748 standard; protein; 90 AA.

XX AC

XX AAY66748;

XX AC

XX 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO1159.

XX DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX OS

XX PN WO9963088-A2.

XX XX

XX PD 09-DEC-1999.

XX XX

XX PF 02-JUN-1999; 99WO-US012252.

XX XX

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 03-JUN-1998; 98US-0087759P.

XX PR 04-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

XX PR 05-JUN-1998; 98US-0088217P.

XX PR 09-JUN-1998; 98US-0088655P.

XX PR 10-JUN-1998; 98US-0088722P.

XX PR 10-JUN-1998; 98US-0088730P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088740P.

XX PR 10-JUN-1998; 98US-0088741P.

XX PR 10-JUN-1998; 98US-0088742P.

XX PR 10-JUN-1998; 98US-0088810P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

26	462	100.0	90	6 ABUS8623	Abus8623 Human sec
27	462	100.0	90	6 ABO34137	Abo34137 Human PRO
28	462	100.0	90	6 ADA45993	Ada45993 Novel hum
29	462	100.0	90	6 ADA76424	Ada76424 Human PRO
30	462	100.0	90	6 ADA19074	Ada19074 Human PRO
31	462	100.0	90	6 ADA61697	Ada61697 Homo sapi
32	462	100.0	90	6 ADB19482	Adb19482 Novel hum
33	462	100.0	90	6 ADB28023	Adb28023 Human PRO
34	462	100.0	90	6 ADA86502	Ada86502 Novel hum
35	462	100.0	90	6 ADB16066	Adb16066 Human PRO
36	462	100.0	90	6 ADA37888	Ada37888 Human sec
37	462	100.0	90	6 ADA47852	Ada47852 Human PRO
38	462	100.0	90	6 ADA21574	Ada21574 Human sec
39	462	100.0	90	6 ADA10361	Ada10361 Human sec
40	462	100.0	90	6 ADA67647	Ada67647 Human PRO
41	462	100.0	90	6 ADB30654	Adb30654 Human PRO
42	462	100.0	90	6 ADA85950	Ada85950 Novel hum
43	462	100.0	90	6 ADA17905	Ada17905 Human PRO
44	462	100.0	90	6 ADA97162	Ada97162 Human PRO
45	462	100.0	90	6 ADA79466	Ada79466 Human PRO

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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
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PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
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PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094551P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095923P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 17-AUG-1998; 98US-0096899P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

( GETH ) GENENTECH INC.
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WF, Yuan J;
XX WPI: 2000-072883/06.
DR N-PSDB; AAZ65094.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX Claim 12; Fig 272; 822pp; English.
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LBL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX Sequence 90 AA;
SQ
Query Match 100.0%; Score 462; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQFTQSSLEDVTPTKAVKTT 60
DB 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQFTQSSLEDVTPTKAVKTT 60
```

QY 61 GKGIVKGRNLDGRGLILGAEAWGRGVKKNT 90
 Db 61 GKGIVKGRNLDGRGLILGAEAWGRGVKKNT 90

RESULT 2
 AAB33469
 ID AAB33469 standard; protein; 90 AA.
 AC AAB33469;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO1159 protein UNQ589 SEQ ID NO:273.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;
 KW antianaemic; hepatotropic; viricide; antipsoriatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; Sjogren's syndrome; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease;
 XX
 OS Homo sapiens.
 XX
 PN WO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US005841.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162508P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030099.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI: 2000-572271/53.
 DR N-PSDB; AAC58634.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 PS Claim 33; Fig 112; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 90 AA;
 Query Match 100.0%; Score 462; DB 3; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTFFLSLLLLLVCEAIWRSNCSNTLENGYFLSRKNHNSOPTQSSLEDSVTPTKAVKTT 60
 Db 1 MTFFLSLLLLLVCEAIWRSNCSNTLENGYFLSRKNHNSOPTQSSLEDSVTPTKAVKTT 60
 QY 61 GKGIVKGRNLDGRGLILGAEAWGRGVKKNT 90
 Db 61 GKGIVKGRNLDGRGLILGAEAWGRGVKKNT 90

RESULT 3
 AAU12408
 ID AAU12408 standard; protein; 90 AA.
 AC AAU12408;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO1159 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX

PN WO200140466-A2.
 XX 07-JUN-2001.
 PD 01-DEC-2000; 2000WO-US032678.
 XX 01-DEC-1999; 99WO-US028301.
 PI 01-DEC-1999; 99WO-US028634.
 PI 02-DEC-1999; 99WO-US028551.
 PI 02-DEC-1999; 99WO-US028564.
 PI 02-DEC-1999; 99WO-US028565.
 PI 09-DEC-1999; 99US-0170262P.
 PI 16-DEC-1999; 99WO-US030095.
 PI 20-DEC-1999; 99WO-US030911.
 PI 20-DEC-1999; 99WO-US030999.
 PI 30-DEC-1999; 99WO-US031243.
 PI 30-DEC-1999; 99WO-US031274.
 PI 05-JAN-2000; 2000WO-US000219.
 PI 06-JAN-2000; 2000WO-US000277.
 PI 06-JAN-2000; 2000WO-US000376.
 PI 11-FEB-2000; 2000WO-US003565.
 PI 18-FEB-2000; 2000WO-US004341.
 PI 18-FEB-2000; 2000WO-US004342.
 PI 22-FEB-2000; 2000WO-US004414.
 PI 24-FEB-2000; 2000WO-US004914.
 PI 24-FEB-2000; 2000WO-US005004.
 PI 01-MAR-2000; 2000WO-US005601.
 PI 02-MAR-2000; 2000WO-US005841.
 PI 03-MAR-2000; 2000US-0187202P.
 PI 10-MAR-2000; 2000WO-US006319.
 PI 15-MAR-2000; 2000WO-US006884.
 PI 20-MAR-2000; 2000WO-US007377.
 PI 21-MAR-2000; 2000WO-US007532.
 PI 30-MAR-2000; 2000WO-US008439.
 PI 17-MAY-2000; 2000WO-US013705.
 PI 22-MAY-2000; 2000WO-US014042.
 PI 30-MAY-2000; 2000WO-US014941.
 PI 02-JUN-2000; 2000WO-US015264.
 PI 05-JUN-2000; 2000US-0209832P.
 PI 28-JUL-2000; 2000WO-US020710.
 PI 11-AUG-2000; 2000WO-US022031.
 PI 23-AUG-2000; 2000WO-US023522.
 PI 24-AUG-2000; 2000WO-US023328.
 PI 08-NOV-2000; 2000WO-US030952.
 PI 10-NOV-2000; 2000WO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX N-PSDB; AAS21480.
 DR WFI; 2001-408281/43.
 DR N-PSDB; AAS21480.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 XX Claim 12; Fig 474; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the

CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 XX Sequence 90 AA;
 Query Match 100.0%; Score 462; DB 4; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKTT 60
 Db 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKTT 60
 QY 61 GKGIVKGNLDSRGLILGAEAWGRGVKKNT 90
 Db 61 GKGIVKGNLDSRGLILGAEAWGRGVKKNT 90
 RESULT 4
 AAB50922
 ID AAB50922 standard; protein; 90 AA.
 XX AC AAB50922;
 XX 21-MAR-2001 (first entry)
 DT Human PRO1159 protein.
 DE
 DE
 XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
 KW antirheumatic; cardiant; antianaemic; immunosuppressive; antihydroid;
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
 KW antiallergic; antiasthmatic; immune related disorder;
 KW hepatobiliary disease; autoimmune disease; allergy.
 XX Homo sapiens.
 XX WC200073452-A2.
 PN 07-DEC-2000.
 PD 02-JUN-2000; 2000WO-US015264.
 PF 02-JUN-1999; 99WO-US012252.
 XX 20-JUL-1999; 99US-0144732P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 28-JUL-1999; 99US-0146222P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 15-SEP-1999; 99WO-US021090.
 XX 15-SEP-1999; 99WO-US021547.
 XX 29-OCT-1999; 99US-0162506P.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1999; 99WO-US028634.
 XX 02-DEC-1999; 99WO-US028551.
 XX 02-DEC-1999; 99WO-US028565.
 XX 09-DEC-1999; 99US-0170262P.
 XX 20-DEC-1999; 99WO-US030911.
 XX 05-JAN-2000; 2000WO-US000219.
 XX 11-FEB-2000; 2000WO-US000376.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 22-FEB-2000; 2000WO-US004414.
 XX 24-FEB-2000; 2000WO-US004914.
 XX 24-FEB-2000; 2000WO-US005004.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;
 PI Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-025253/03.
 DR N-PSDB; AAC91481.
 XX
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful in
 PT the diagnosis and treatment of immune related disorders, e.g. systemic
 PT lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis
 PT and diabetes mellitus.
 XX
 XX Claim 58; Fig 42; 218pp; English.
 PS
 XX
 XX The present sequence is one of thirty three novel PRO polypeptides. The
 CC PRO polypeptides, anti-PRO antibodies, agonists and antagonists are
 CC useful for treating and diagnosing immune related disorders such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis,
 CC idiopathic inflammatory myopathies, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, demyelinating diseases of the central and peripheral nervous
 CC systems (such as multiple sclerosis, idiopathic demyelinating
 CC demyelinating polyneuropathy), Guillain-Barre syndrome, and chronic inflammatory
 CC polynuropathy or Guillain-Barre syndrome, and chronic inflammatory
 CC infectious, autoimmune chronic active hepatitis, primary biliary
 CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity and urticaria), immunological diseases of the lung
 CC (such as eosinophilic pneumonia), idiopathic pulmonary fibrosis and
 CC hypersensitivity pneumonitis), transplantation associated diseases
 CC including graft rejection and graft-versus-host diseases
 XX
 XX Sequence 90 AA;
 PT
 PT Query Match 100.0%; Score 462; DB 4; Length 90;
 PT Best Local Similarity 100.0%; Pred. No. 9.8e-49;
 XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PS
 XX 1 MTFFLSLLLLVCEAIWRNSGNTLNGVFLSRNKENHSQPTQSSLEDSVPTKAVKTT 60
 CC |||||
 Db 1 MTFFLSLLLLVCEAIWRNSGNTLNGVFLSRNKENHSQPTQSSLEDSVPTKAVKTT 60
 CC |||||
 QY 61 GKGIVKGRNLDGRGLILGAEAWGRGVKNT 90
 CC |||||
 Db 61 GKGIVKGRNLDGRGLILGAEAWGRGVKNT 90
 CC |||||
 RESULT 5
 AAB65271
 ID AAB65271 standard; protein; 90 AA.
 XX
 AC AAB65271;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1159 (UNQ589) protein sequence SEQ ID NO:377.
 XX
 XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW

KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX Homo sapiens.
 OS
 XX WO200073454-A1.
 PN
 XX
 XX 07-DEC-2000.
 PD
 XX
 XX 30-MAR-2000; 2000WO-US008439.
 PF
 XX
 XX 02-JUN-1999; 99WO-US012252P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44240.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX
 XX Claim 12; Fig 272; 935pp; English.
 PS
 XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 XX Sequence 90 AA;
 SQ
 Query Match 100.0%; Score 462; DB 4; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  GKGIKGRNLDRLGLILGAAGRGVKKNT 90

RESULT 6
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ID  ABU58086 standard; protein; 90 AA.
AC  ABU58086;
XX
DT  14-APR-2003 (first entry)
DE  Human PRO polypeptide #118.
XX
KW  Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW  horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW  antibody-dependent enzyme mediated prodrug therapy.
XX
OS  Homo sapiens.
XX
FN  US2003027163-A1.
XX
PD  06-FEB-2003.
XX
PF  15-NOV-2001; 2001US-00997666.
XX
PR  16-JUN-1997; 97US-0049787P.
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PR  13-NOV-1997; 97US-0065311P.
PR  24-NOV-1997; 97US-0066770P.
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PR  07-JUL-1998; 98US-0091982P.
PR  09-JUL-1998; 98US-0092182P.
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PR  17-AUG-1998; 98US-0096895P.
PR  17-AUG-1998; 98US-0096897P.
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PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098252P.
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PR 16-SEP-1998; 98US-0100634P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 07-OCT-1998; 98US-0100858P.
PR 01-DEC-1998; 98US-0100858P.
PR 22-DEC-1998; 98US-0100858P.
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PR 08-MAR-1999; 98US-0100858P.
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PR 23-JUN-1999; 98US-0100858P.
PR 07-JUL-1999; 98US-0100858P.
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PR 22-FEB-2000; 98US-0100858P.
PR 24-FEB-2000; 98US-0100858P.
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PR 10-MAR-2000; 98US-0100858P.
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PR 20-MAR-2000; 98US-0100858P.
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PR 15-MAY-2000; 98US-0100858P.
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PR 28-JUL-2000; 98US-0100858P.
PR 11-AUG-2000; 98US-0100858P.
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Query Match 100.0%; Score 462; DB 6; Length 90;
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GKGIYKGRNLDGRGLILGAEAWGRGVKNT 90

RESULT 7
ABUS9164
ID ABUS9164 standard; protein; 90 AA.
XX
AC ABUS9164;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO1159.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97US-0062250P.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
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PR 03-JUN-1998; 98US-0087759P.
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PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 12-JUN-1998; 98US-0089105P.
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PR 02-JUN-1999; 99WO-US012252.
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PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
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PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerecht ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kijavir IU, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX WPI; 2003-247083/24.
DR N-PSDB; ABX80363.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX

PS Claim 12; Fig 272; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth. and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 90 AA;
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKTT 60
Db 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKTT 60
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RESULT 8
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ID ABU82676 standard; protein; 90 AA.
XX
XX ABU82676;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human secreted/transmembrane protein PRO1159.
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX cardiac insufficiency disorders; angiogenesis; wound healing;
XX cancerous tumour; immune response; retinal disorder; sight loss;
XX retinitis pigmentosum; age-related macular degeneration; AMD;
XX kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
XX Crohn's disease; sports injury; arthritis.
XX
XX Homo sapiens.
XX
XX US2003032023-A1.
XX
XX 13-FEB-2003.
XX
XX 14-NOV-2001; 2001US-00990711.
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XX 16-JUN-1997; 97US-0049787P.


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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
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PR 30-NOV-1999; 99WO-US028313.
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PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004914.
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PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.

Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred.No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFLLSLLLIVCAIRWSNGSNTLENGYFLSRKNKHNSQTSLSLSDSVTPPKAVKTT 60
DB 1 MTFLLSLLLIVCAIRWSNGSNTLENGYFLSRKNKHNSQTSLSLSDSVTPPKAVKTT 60

QY 61 GKGIVKGRNLDRLGILGAEAWGRGVKKNT 90
DB 61 GKGIVKGRNLDRLGILGAEAWGRGVKKNT 90

RESULT 9
AB017852
ID AB017852 standard; protein; 90 AA.
XX
AC AB017852;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1159.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antididiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
FN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX

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PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022931.
PR 29-OCT-1998; 98WO-US022932.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005130.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005024.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.

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PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-08972035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-0887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-09098827.
PR 06-AUG-2001; 2001US-09224419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2003-341980/32.
DR N-PSDB; ACD24089.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 474; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KY 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSQPTQSSLESVPTKAVKTT 60

Db 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSQPTQSSLESVPTKAVKTT 60
QY 61 GKGIKGRNLDNRGLILGAEAWGRGVKKNT 90
Db 61 GKGIKGRNLDNRGLILGAEAWGRGVKKNT 90
RESULT 10
ABU60595
ID ABU60595 standard; protein; 90 AA.
AC ABU60595;
XX
XX 01-MAY-2003 (first entry)
XX Human secreted/transmembrane protein, #154.
DE Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX Homo sapiens.
XX US2002160384-A1.
XX 31-OCT-2002.
XX
XX 14-NOV-2001; 2001US-00992598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.

PR 05-JUN-1998; 98US-0088212P.
 PR 09-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089601P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 (GETH) GENENTECH LTD.
 PA Ashkenazi A7, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 GRIMALDI JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 ROY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 ZHANG Z;
 WPI; 2003-102117/09.
 N-PSDB; ABX64187.
 Novel secreted and transmembrane polypeptide for modulating biological
 activity of cell expressing the polypeptide, identifying agonists or
 antagonists of polypeptide, and as molecular weight markers.
 Claim 12; Fig 272; 649pp; English.
 The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The PRO
 polypeptides are secreted and transmembrane proteins. The PRO
 polypeptides are useful for detecting other PRO polypeptides, for linking
 bioactive molecules to cells expressing PRO polypeptides, for modulating
 biological activities of cells expressing PRO polypeptides, and for
 identifying agonists or antagonists. The polynucleotide sequences
 encoding PRO polypeptides are useful as hybridisation probes, in
 chromosome and gene mapping, in the generation of antisense RNA and DNA,
 in the preparation of PRO polypeptides, for generating transgenic animals
 or knockout animals, to construct hybridisation probes for mapping the
 gene which encodes the PRO polypeptide, and for the genetic analysis of
 individuals with genetic disorders, in gene therapy, for chromosome
 identification, as chromosome markers, and for generating probes for PCR,
 Northern analysis, Southern analysis and Western analysis. ABU13860-
 CC ABU14006 represent the human PRO polypeptides of the invention. Note: The
 CC sequence data for this patent was obtained in electronic format directly
 CC from the USPTO web site at seqdata.uspto.gov/paipedEntry.html
 XX
 SQ Sequence 90 AA;
 Query Match 100.0%; Score 462; DB 6; Length 90;
 Best Local Similarity 100.0%; Pred.No. 9.8e-45;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTFELSLILLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKTT 60
 DB 1 MTFELSLILLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKTT 60
 QY 61 GKGIVKGNLDSRGLILGAEGAWGRGVKNT 90
 DB 61 GKGIVKGNLDSRGLILGAEGAWGRGVKNT 90
 RESULT 12
 ABU81106
 ID ABU81106 standard; protein; 90 AA.
 XX
 AC ABU81106;
 XX 23-JUN-2003 (first entry)
 XX Human PRO polypeptide #237.
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiomet;
 KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.
 OS Homo sapiens.
 XX
 XX US2003004311-A1.
 XX
 XX 02-JAN-2003.
 XX
 XX 19-DEC-2001; 2001US-00028072.
 XX

RESULT 13
ABU72562
ID ABU72562 standard; protein; 90 AA.
XX AC ABU72562;
XX DT 17-JUN-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1159.
XX KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;
XX KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening.
XX OS Homo sapiens.
XX PN US2003003531-A1.
XX PD 02-JAN-2003.
XX PF 19-NOV-2001; 2001US-00989734.
XX PR 16-JUN-1997; 97US-00497872.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
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PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
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PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-352829/33.
DR N-PSDB; ACA64409.
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX Claim 12; Fig 272; 663pp; English.
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's

CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide

XX Sequence 90 AA;

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Best Local Similarity 100.0%; Pred. No. 9,8e-49;
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ABU66806
ID ABU66806 standard; protein; 90 AA.

XX AC ABU66806;

XX DT 23-MAY-2003 (first entry)

XX DE Human PRO polypeptide #237.

XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX OS Homo sapiens.

XX US2003036180-A1.

XX PD 20-FEB-2003.

XX PF 09-MAY-2002; 2002US-00143114.

XX PF 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022591.

PR 29-OCT-1998; 98WO-US022592.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
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PR 06-JAN-2000; 2000WO-US000277.
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PR 11-FEB-2000; 2000WO-US003565.
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PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
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PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
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PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
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PR 01-JUN-2001; 2001US-00872035.
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PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
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PR 19-DEC-2001; 2001US-00028072.

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XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Bersini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
XX DR N-PSDB; ACA03839.
XX
XX PT New secreted and transmembrane PRO nucleic acids, useful for gene
XX PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
XX PT typing, and in chromosome identification.
XX PS Claim 12; Fig 474; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. NOTE: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipdsIDentry.html
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XX SQ Sequence 90 AA;
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 GKGIKGRNLDRLGLLGAWGRGVKNT 90
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XX AC ABU59887;
XX DT 13-MAY-2003 (first entry)
XX DE Novel secreted and transmembrane protein PRO1159.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX KW cardiac insufficiency disorder; cancer; tumour; immune response;
XX KW adrenal cortical capillary endothelial growth; c-fos induction;
XX KW vascular endothelial growth factor inhibition; VEGF inhibition;
XX KW endothelial cell growth inhibitor; T-lymphocyte stimulation;
XX KW retinal neurons cell survival; rod photoreceptor cell survival;
XX KW retinal disorder; retinitis pigmentosa; kidney disease;
XX KW mammalian kidney mesangial cell proliferation; Berger disease;
XX KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.

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PN US2003017563-A1.
XX
XX PD 23-JAN-2003.
XX
XX PF 07-MAY-2002; 2002US-00140808.
XX
XX PR 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
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XX PR 05-JAN-2000; 2000WO-US000219.
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XX PR 02-MAR-2000; 2000WO-US005746.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 10-MAR-2000; 2000WO-US006319.
XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 20-MAR-2000; 2000WO-US007377.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 30-MAR-2000; 2000WO-US008439.
XX PR 17-MAY-2000; 2000WO-US013705.
XX PR 22-MAY-2000; 2000WO-US014042.
XX PR 30-MAY-2000; 2000WO-US014941.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 11-AUG-2000; 2000WO-US022031.
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XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 08-NOV-2000; 2000WO-US030952.

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GenCore version 5.1.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17


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; PRIOR APPLICATION NUMBER: 60/091360
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Descrochers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Feng, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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RESULT 3
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; Sequence 377, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020072497A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301065
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; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 377, Application US/0989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC70
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GKGIVKGRNLDNRGLILGAEAWGRGVKNT 90
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RESULT 7
US-09-991-073-377 Application US/09991073
; Sequence 377 Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
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 ; TITLE OF INVENTION: Acids Encoding the Same
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140 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;
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; Sequence 377, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
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 ; Sequence 377, Application US/09990456
 ; Patent No. US20020137890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Inc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
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 ; APPLICANT: Wood, William I.
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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.6e-47;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTFLLSLLLLVCEAIWRNSGNTLENGYFLSRNKNHSQPTQSSLEDSVTTKAVKTT 60
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 Qy 61 GKGVKGRNLDNRGLILGAEAWGRGVKNT 90
 Db 61 GKGVKGRNLDNRGLILGAEAWGRGVKNT 90

RESULT 12

US-09-989-721-377
Sequence 377, Application US/09989721

Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C55
CURRENT APPLICATION NUMBER: US/09/989, 721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.6e-47;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFLLSLLLVCETWRSNGNTLNGVFLSRNKNHSHQPTQSSLEDSTVTPKAVKTT 60

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Db 61 GKGVKGRNLDLSRGLILGAAWGRGVKNT 90

RESULT 13

US-09-992-598-377
; Sequence 377, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.6e-47;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFPLSLLLLVCEAIWRNSGNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTT 60

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Qy 61 GKGVKGRNLDLSRGLILGAEGWGRGVKNT 90

Db 61 GKGVKGRNLDLSRGLILGAEGWGRGVKNT 90

RESULT 14

US-09-989-293A-377

; Sequence 377, Application US/09989293A

; Patent No. US20020177164A1

```

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
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; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
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; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24

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; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
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; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFPLSLLLLVCEAIWRSGNSNTLENGYFLSRNKENHSQPTOSSLEDSVTPTKAVKTT 60
Db 1 MTFPLSLLLLVCEAIWRSGNSNTLENGYFLSRNKENHSQPTOSSLEDSVTPTKAVKTT 60

Qy 61 GKGIVKGRNLDLSRGLILGAEGAWGRGVKNT 90
Db 61 GKGIVKGRNLDLSRGLILGAEGAWGRGVKNT 90

RESULT 15
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; Sequence 377, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: 60/049787
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
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6	PRIOR APPLICATION NUMBER: 60/090444	
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10	PRIOR APPLICATION NUMBER: 60/090472	
11	PRIOR FILING DATE: 1998-06-24	
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14	PRIOR APPLICATION NUMBER: 60/090540	
15	PRIOR FILING DATE: 1998-06-24	
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22	PRIOR APPLICATION NUMBER: 60/090678	
23	PRIOR FILING DATE: 1998-06-25	
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27	PRIOR FILING DATE: 1998-06-25	
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31	PRIOR FILING DATE: 1998-06-25	
32	PRIOR APPLICATION NUMBER: 60/090862	
33	PRIOR FILING DATE: 1998-06-26	
34	PRIOR APPLICATION NUMBER: 60/090863	
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44	PRIOR APPLICATION NUMBER: 60/091626	
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46	PRIOR APPLICATION NUMBER: 60/091633	
47	PRIOR FILING DATE: 1998-07-02	
48	PRIOR APPLICATION NUMBER: 60/091978	
49	PRIOR FILING DATE: 1998-07-07	
50	PRIOR APPLICATION NUMBER: 60/091982	
51	PRIOR FILING DATE: 1998-07-07	
52	PRIOR APPLICATION NUMBER: 60/092182	
53	PRIOR FILING DATE: 1998-07-09	

Query Match	100.0%;	Score 462;	DB 9;	Length 90;
Best Local Similarity	100.0%;	Pred. No. 1.6e-47;		
Matches	90.	Conservative	0.	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy
61 GKGI VKGRNLD SRGL ILGAEAWGRGVKNT 90

Dδ
61 GKGI VKGRNLD SRGL ILGAEAWGRGVKNT 90

Search completed: March 31, 2004, 12:20:39
Job time : 41 secs